

RL J. CELL SCI. 106:909-918(1993).
DR EMBL: L21838: G474949;
SQ SEQUENCE 400 AA; 46147 MW; 7540DE80 CRC32;

Query Match 74.0%; Score 54; DB 3: Length 400;
Best Local Similarity 80.0%;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 325 LERKLODADHN 334
QY 1 LRRKLODVHN 10

Search completed: Thu Jul 30 11:11:48 1998
Job time : 29 secs.

MIPS

(TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:00:59 1998; Maspar time 4.06 Seconds
Molecular output not generated. 83.029 Million cell updates/sec

Title: >US-08-817-547A-3
Description: (1-8) from US08817547A.pep
Perfect Score: 54
Sequence: 1 SVSEIQLM 8

Scoring table: PAM 150
Gap 15

Searched: 140542 segs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 21.157; Variance 18.924; scale 1.118

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	50	92.6	105	10	063473	PARATHYROID HORMONE (F	5.43e+02
2	45	83.3	1405	10	P70366	STERIOD RECEPTOR COACT	1.44e+00
3	45	83.3	1405	10	061202	STERIOD RECEPTOR COACT	1.44e+00
4	45	83.3	1441	2	000150	STERIOD RECEPTOR COACT	1.44e+00
5	45	83.3	1447	10	P70365	NUCLEAR RECEPTOR CO-AC	1.44e+00
6	44	81.5	248	9	008320	ACETYLGLUTAMATE KINASE	2.68e+00
7	43	79.6	167	9	P66578	YDAE PROTEIN.	4.96e+00
8	43	79.6	910	11	011421	HEXON PROTEIN.	4.96e+00
9	43	79.6	911	11	083905	TERMINAL PROTEIN.	4.96e+00
10	42	77.8	418	3	026662	VERY EARLY BLASTULA PR	9.08e+00
11	41	75.9	248	8	004682	PT16.	1.64e+01
12	41	75.9	276	3	021996	SIMILAR TO TYROSINE KI	1.64e+01
13	41	75.9	373	9	049979	CORA.	1.64e+01
14	41	75.9	481	10	060823	THYMOMA VIRAL PROTO-ON	1.64e+01
15	41	75.9	591	2	013026	65 KDA HYDROPHOBIC PRO	1.64e+01
16	41	75.9	591	2	000553	FOLATE CARRIER.	1.64e+01
17	41	75.9	896	9	055544	HYPOTHETICAL 100.3 KD	1.64e+01
18	41	75.9	1371	9	P73337	SENSORY TRANSDUCTION H	1.64e+01
19	41	75.9	3456	11	P89201	POLYPROTEIN.	1.64e+01
20	40	74.1	99	9	Q58911	HYPOTHETICAL 11.5 KD P	2.93e+01

RESULT	ID	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	063473	92.6	105	10	063473	PARATHYROID HORMONE (F	5.43e+02	2.93e+01
2	45	83.3	1405	10	P70366	STERIOD RECEPTOR COACT	1.44e+00	2.93e+01
3	45	83.3	1405	10	061202	STERIOD RECEPTOR COACT	1.44e+00	2.93e+01
4	45	83.3	1441	2	000150	STERIOD RECEPTOR COACT	1.44e+00	2.93e+01
5	45	83.3	1447	10	P70365	NUCLEAR RECEPTOR CO-AC	1.44e+00	2.93e+01
6	44	81.5	248	9	008320	ACETYLGLUTAMATE KINASE	2.68e+00	2.93e+01
7	43	79.6	167	9	P66578	YDAE PROTEIN.	4.96e+00	2.93e+01
8	43	79.6	910	11	011421	HEXON PROTEIN.	4.96e+00	2.93e+01
9	43	79.6	911	11	083905	TERMINAL PROTEIN.	4.96e+00	2.93e+01
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14	41	75.9	481	10	060823	THYMOMA VIRAL PROTO-ON	1.64e+01	2.93e+01
15	41	75.9	591	2	013026	65 KDA HYDROPHOBIC PRO	1.64e+01	2.93e+01
16	41	75.9	591	2	000553	FOLATE CARRIER.	1.64e+01	2.93e+01
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19	41	75.9	3456	11	P89201	POLYPROTEIN.	1.64e+01	2.93e+01
20	40	74.1	99	9	Q58911	HYPOTHETICAL 11.5 KD P	2.93e+01	2.93e+01

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	063473	92.6	105	10	063473	PARATHYROID HORMONE (F	5.43e+02	2.93e+01
2	45	83.3	1405	10	P70366	STERIOD RECEPTOR COACT	1.44e+00	2.93e+01
3	45	83.3	1405	10	061202	STERIOD RECEPTOR COACT	1.44e+00	2.93e+01
4	45	83.3	1441	2	000150	STERIOD RECEPTOR COACT	1.44e+00	2.93e+01
5	45	83.3	1447	10	P70365	NUCLEAR RECEPTOR CO-AC	1.44e+00	2.93e+01
6	44	81.5	248	9	008320	ACETYLGLUTAMATE KINASE	2.68e+00	2.93e+01
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9	43	79.6	911	11	083905	TERMINAL PROTEIN.	4.96e+00	2.93e+01
10	42	77.8	418	3	026662	VERY EARLY BLASTULA PR	9.08e+00	2.93e+01
11	41	75.9	248	8	004682	PT16.	1.64e+01	2.93e+01
12	41	75.9	276	3	021996	SIMILAR TO TYROSINE KI	1.64e+01	2.93e+01
13	41	75.9	373	9	049979	CORA.	1.64e+01	2.93e+01
14	41	75.9	481	10	060823	THYMOMA VIRAL PROTO-ON	1.64e+01	2.93e+01
15	41	75.9	591	2	013026	65 KDA HYDROPHOBIC PRO	1.64e+01	2.93e+01
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17	41	75.9	896	9	055544	HYPOTHETICAL 100.3 KD	1.64e+01	2.93e+01
18	41	75.9	1371	9	P73337	SENSORY TRANSDUCTION H	1.64e+01	2.93e+01
19	41	75.9	3456	11	P89201	POLYPROTEIN.	1.64e+01	2.93e+01
20	40	74.1	99	9	Q58911	HYPOTHETICAL 11.5 KD P	2.93e+01	2.93e+01

Thu Jul 30 13:38:11 1998

US-08-817-547A-3.rpt

DR EMBL; U64828; G1490876; -
SQ SEQUENCE 1405 AA; 152644 MW; 1743E755 CRC32;

Query Match

Best Local Similarity 83.38; Score 45; DB 10; Length 1405;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 73 TVDQIQLM 80

OY 1 SVSEIQLM 8

Search completed: Thu Jul 30 10:01:39 1998
Job time : 40 secs.

 MIPSE
 (TW)

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MSPrch_DP protein - protein database search, using Smith-Waterman algorithm
 on: Thu Jul 30 10:05:09 1998; MasPar time 2.56 Seconds
 Molecular output not generated. 41.911 Million cell updates/sec

Title: >US-08-817-547A-4
 Description: (1-7) from US08817547A.pep
 Perfect Score: 43
 Sequence: 1 SVSEIQL 7

Scoring table: PAM 150
 Gap 15

Searched: 124785 segs, 15338987 residues
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-geneseq31-2
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27

Statistics: Mean 13.853; Variance 40.505; scale 0.342

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	43	100.0	16 25	W21948	Fusion protein compri	9.43e+01
2	43	100.0	20 25	W21947	Fusion protein compri	9.43e+01
3	43	100.0	33 3	P82176	Sequence of parathyro	9.43e+01
4	43	100.0	34 22	W17949	Human parathyroid hor	9.43e+01
5	43	100.0	34 23	W24273	Wild type parathyroid	9.43e+01
6	43	100.0	34 23	W08131	Human PTH derivative,	9.43e+01
7	43	100.0	34 23	W08130	Human PTH derivative,	9.43e+01
8	43	100.0	34 9	R58232	[Lys32]-hPTH(1-34)-NH	9.43e+01
9	43	100.0	34 7	R34356	Human parathyroid hor	9.43e+01
10	43	100.0	34 7	R34357	Human parathyroid hor	9.43e+01
11	43	100.0	34 9	R58054	[L8,A17,Q18,A19,R22,T	9.43e+01
12	43	100.0	34 9	R58195	[S14,I15,Q16,D17,L18,	9.43e+01
13	43	100.0	34 3	P50517	Sequence of methionin	9.43e+01
14	43	100.0	34 8	R41549	[D-Ser3]hPTH (1-34)NH	9.43e+01
15	43	100.0	34 8	R41551	[Thr16]hPTH (1-34).	9.43e+01
16	43	100.0	34 22	W17966	Cyclised human parath	9.43e+01
17	43	100.0	34 22	W17968	Human PTH analogue [C	9.43e+01
18	43	100.0	34 22	W17968	Human parathyroid hor	9.43e+01
19	43	100.0	35 14	R74504	Parathyroid hormone p	9.43e+01

20	43	100.0	35 14	R74503	Parathyroid hormone p	9.43e+01
21	43	100.0	35 14	R74510	Parathyroid hormone p	9.43e+01
22	43	100.0	35 14	R74509	Parathyroid hormone p	9.43e+01
23	43	100.0	35 14	R74426	Parathyroid hormone p	9.43e+01
24	43	100.0	35 14	R74425	Parathyroid hormone p	9.43e+01
25	43	100.0	36 9	R58212	[Ala17]-hPTH(1-36)-NH	9.43e+01
26	43	100.0	36 9	R58046	[L8,A16,D17,L18,A19]-	9.43e+01
27	43	100.0	36 9	R58278	[D-Met18]-hPTH(1-36)-	9.43e+01
28	43	100.0	36 9	R58277	[Nle18]-hPTH(1-36)-NH	9.43e+01
29	43	100.0	36 9	R58196	[D-Phe34, D-Ala36]-hp	9.43e+01
30	43	100.0	36 9	R58055	[L8,Q18]-hPTH(1-36)-O	9.43e+01
31	43	100.0	36 9	R58227	[D-Gln29]-hPTH(1-36)-	9.43e+01
32	43	100.0	36 9	R58213	[D-Ser17]-hPTH(1-36)-	9.43e+01
33	43	100.0	36 9	R58214	[Ala19]-hPTH(1-36)-NH	9.43e+01
34	43	100.0	38 9	R58134	[Ile19]-hPTH(1-38)-OH	9.43e+01
35	43	100.0	38 9	R58141	[Leu21]-hPTH(1-38)-OH	9.43e+01
36	43	100.0	38 9	R58105	[Val14]-hPTH(1-38)-OH	9.43e+01
37	43	100.0	38 9	R58158	[Ala27]-hPTH(1-38)-OH	9.43e+01
38	43	100.0	44 26	P30015	Human parathyroid hor	9.43e+01
39	43	100.0	47 25	W21946	Fusion protein compri	9.43e+01
40	43	100.0	84 27	W25687	Human parathyroid hor	9.43e+01
41	43	100.0	84 25	W29420	Human parathyroid hor	9.43e+01
42	43	100.0	84 4	R23378	Bovine parathyroid ho	9.43e+01
43	43	100.0	84 8	R42072	Stability-enhanced hu	9.43e+01
44	43	100.0	84 5	R29565	Oxidation resistant [9.43e+01
45	43	100.0	84 5	R29563		

ALIGNMENTS

RESULT 1
 ID W21948 standard; Protein; 16 AA.
 AC W21948;
 DT 30-JAN-1998 (first entry)
 DE Fusion protein comprising linker and PTH 1-37 (residues 1-7).
 KW Linker: parathyroid hormone 1-37; PTH 1-37; streptavidin;
 KW fusion protein; recombinant production; TEV N1a protease;
 KW tobacco etch virus.
 OS Synthetic.
 OS Homo sapiens.
 FT Key
 FT Peptide 1.1
 FT /note= "Met(13-139) streptavidin residue"
 FT Peptide 2.9
 FT /note= "linker cleavable by TEV N1a protease"
 FT Peptide 10.16
 FT /note= "parathyroid hormone 1-37 (residues 1-7)"
 PN W09718314-A1.
 PD 22-MAY-1997.
 PF 06-NOV-1996; E04850.
 PR 16-NOV-1995; DE-042702.
 PA (BOE) BOEHRINGER MANNHEIM GMBH.
 PI Kopetzki E;
 DR WPI: 97-289290/26.
 DR N-PSDB: T73912.
 PT Recombinant production of peptide(s) as fusions with streptavidin
 PT attached via cleavable linker - especially for utroctropin and
 PT parathyroid hormone production.
 PS Example 4; Fig 3; 37pp; German.
 CC The DNA encoding the present sequence, a linker and residues 1-7 of
 CC the parathyroid hormone 1-37 (PTH 1-37) peptide with codon usage
 CC optimised for E. coli, was ligated to the 2.9 kb NheI-HindIII
 CC fragment of pSAM-CORE, which contains the Met(13-139) streptavidin
 CC (SA) sequence, to give pSA-TEV-PTH. pSA-TEV-PTH and the LacIQ
 CC repressor plasmid PUBS500 were used to transform E. coli K12 RM82.
 CC The transformants were grown, with IPTG induction, in medium
 CC containing kanamycin and ampicillin. Cells were harvested, lysed
 CC and isolated inclusion bodies solubilised in guanidine
 CC hydrochloride, and renatured by dilution in pH 7 phosphate buffer.
 CC The solution was clarified and the supernatant concentrated and
 CC purified on a column of immobilised immunoblotin. The purified
 CC material was incubated with tobacco etch virus (TEV) N1a protease
 CC and the PTH 1-37 fragment released, recovered by SA fragment

CC removal on an iminobiotin column followed by chromatography on a
 CC fractogel and reverse phase HPLC.
 SQ Sequence 16 AA;

Query Match 100.0%; Score 43; DB 25; Length 16;
 Best Local Similarity 100.0%; Pred. NO. 9.43e+01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 svseql 16
 |||||
 OY 1 SVSEIQL 7

RESULT 2

ID W21947 standard; Protein: 20 AA.

AC W21947;

DT 30-JAN-1998 (first entry)

DE Fusion protein comprising linker and PTH 1-37 (residues 1-7).

Linker: parathyroid hormone 1-37; PTH 1-37; streptavidin;

fusion protein; recombinant production; thrombin.

Synthetic.

OS Homo sapiens.

FH Key

FT Peptide

Location/Qualifiers

1..1

FT Peptide

/note- "Met(13-139) streptavidin residue"

FT Peptide

/note- "linker cleavable by thrombin"

FT Peptide

14..20

FT Peptide

/note- "parathyroid hormone 1-37 (residues 1-7)"

PN MO9718314-A1.

PD 22-MAY-1997.

PF 06-NOV-1996; E04850.

PR 16-NOV-1995; DE-042702.

PA (BOEF) BOEHRINGER MANNHEIM GMBH.

PI Kopetzki E;

DR WPI: 97-289290/26.

DR N-PSDB: T73911.

PT Recombinant production of peptide(s) as fusions with streptavidin

PT attached via cleavable linker - especially for urotropin and

PT parathyroid hormone production

PS Example 3; Fig 3; 37pp; German.

CC The DNA encoding the present sequence, a linker and residues 1-7 of

CC the parathyroid hormone 1-37 (PTH 1-37) peptide with codon usage

CC optimised for E. coli, was ligated to the 2.9 kb NheI-HindIII

CC (SA) sequence, to give PSA-THRO-PTH. PSA-THRO-PTH and the Lactig

CC repressor plasmid PUBS500 were used to transform E. coli K12 RM82.

CC The transformants were grown, with IPTG induction, in medium

CC containing kanamycin and ampicillin. Cells were harvested, lysed

CC and isolated inclusion bodies solubilised in guanidine

CC hydrochloride, and renatured by dilution in pH 7 phosphate buffer.

CC The solution was clarified and the supernatant concentrated and

CC purified on a column of immobilised iminobiotin. The purified

CC material was incubated with thrombin and the PTH 1-37 fragment

CC released, recovered by SA fragment removal on an iminobiotin

CC column followed by chromatography on a fractogel and reverse phase

CC HPLC.

SQ Sequence 20 AA;

Query Match 100.0%; Score 43; DB 25; Length 20;
 Best Local Similarity 100.0%; Pred. NO. 9.43e+01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 14 svseql 20
 |||||
 OY 1 SVSEIQL 7

Search completed: Thu Jul 30 10:05:25 1998
 Job time : 16 secs.

W D S E I Q L (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:04:35 1998; Maspar time 3.05 Seconds
Molecular output not generated. 83.806 Million cell updates/sec

Title: >US-08-817-547A-4
Description: (1-7) from US08817547A.pep
Perfect Score: 43
Sequence: 1 SVSEIQL 7

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r56
1:p1r1 2:p1r2 3:p1r3 4:p1r4 5:nr13d

Statistics: Mean 19.518; Variance 19.793; scale 0.986

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	43	100.0	34	5	1H7H cyclic parathyroid ho	2.97e+00
2	43	100.0	34	5	12WA parathyroid hormone (2.97e+00
3	43	100.0	37	5	1H7H parathyroid hormone f	2.97e+00
4	43	100.0	115	1	PTB6 parathyroid hormone p	2.97e+00
5	43	100.0	115	1	PTH0 parathyroid hormone p	2.97e+00
6	41	95.3	115	2	A05091 parathyroid hormone p	9.26e+00
7	41	95.3	896	2	S76064 parathyroid hormone p	9.26e+00
8	41	95.3	896	2	S59990 parathyroid hormone p	9.26e+00
9	39	90.7	36	5	12WA parathyroid hormone (2.77e+01
10	39	90.7	105	2	151851 parathyroid hormone -	2.77e+01
11	39	90.7	567	2	C69611 ABC transporter regul	2.77e+01
12	39	90.7	1827	2	A35694 cutl protein - f1ssio	4.72e+01
13	38	88.4	119	2	A34937 parathyroid hormone p	4.72e+01
14	38	88.4	958	2	S47179 parathyroid hormone p	4.72e+01
15	38	88.4	3124	2	A40020 collagen alpha 1(XII)	4.72e+01
16	37	86.0	312	2	S66952 hypothetical protein	7.96e+01
17	37	86.0	407	2	B64311 collagenase p1C homo	7.96e+01
18	37	86.0	436	5	3MINA2 nitrogennase (EC 1.18.	7.96e+01
19	37	86.0	436	5	2MINA2 nitrogennase (EC 1.18.	7.96e+01
20	37	86.0	437	5	1MINC2 nitrogennase (EC 1.18.	7.96e+01
21	37	86.0	437	5	3MINC2 nitrogennase (EC 1.18.	7.96e+01
22	37	86.0	437	5	2MINC2 nitrogennase (EC 1.18.	7.96e+01
23	37	86.0	437	5	1MINA2 nitrogennase (EC 1.18.	7.96e+01

24	37	86.0	438	2	A55070	DNA primase (EC 2.7.7	7.96e+01
25	37	86.0 <td>478<th>5</th><th>1N2CC</th><th>nitrogennase molybdenu</th><th>7.96e+01</th></td>	478 <th>5</th> <th>1N2CC</th> <th>nitrogennase molybdenu</th> <th>7.96e+01</th>	5	1N2CC	nitrogennase molybdenu	7.96e+01
26	37	86.0 <td>478<th>1</th><th>1N2CA</th><th>nitrogennase molybdenu</th><th>7.96e+01</th></td>	478 <th>1</th> <th>1N2CA</th> <th>nitrogennase molybdenu</th> <th>7.96e+01</th>	1	1N2CA	nitrogennase molybdenu	7.96e+01
27	37	86.0 <td>492<th>1</th><th>1N2WA</th><th>nitrogennase (EC 1.18.</th><th>7.96e+01</th></td>	492 <th>1</th> <th>1N2WA</th> <th>nitrogennase (EC 1.18.</th> <th>7.96e+01</th>	1	1N2WA	nitrogennase (EC 1.18.	7.96e+01
28	37	86.0 <td>605<th>2</th><th>S36592</th><th>El protein - human pa</th><th>7.96e+01</th></td>	605 <th>2</th> <th>S36592</th> <th>El protein - human pa</th> <th>7.96e+01</th>	2	S36592	El protein - human pa	7.96e+01
29	37	86.0 <td>615<th>2</th><th>A05269</th><th>collagen alpha 1(III)</th><th>7.96e+01</th></td>	615 <th>2</th> <th>A05269</th> <th>collagen alpha 1(III)</th> <th>7.96e+01</th>	2	A05269	collagen alpha 1(III)	7.96e+01
30	37	86.0 <td>764<th>2</th><th>A49448</th><th>irregular chiasm C-to</th><th>7.96e+01</th></td>	764 <th>2</th> <th>A49448</th> <th>irregular chiasm C-to</th> <th>7.96e+01</th>	2	A49448	irregular chiasm C-to	7.96e+01
31	37	86.0 <td>1116<th>2</th><th>S41915</th><th>DNA-directed RNA poly</th><th>7.96e+01</th></td>	1116 <th>2</th> <th>S41915</th> <th>DNA-directed RNA poly</th> <th>7.96e+01</th>	2	S41915	DNA-directed RNA poly	7.96e+01
32	37	86.0 <td>1132<th>2</th><th>JC4127</th><th>protein-tyrosine kina</th><th>7.96e+01</th></td>	1132 <th>2</th> <th>JC4127</th> <th>protein-tyrosine kina</th> <th>7.96e+01</th>	2	JC4127	protein-tyrosine kina	7.96e+01
33	36	83.7 <td>115<th>2</th><th>JC4202</th><th>parathyroid hormone -</th><th>1.32e+02</th></td>	115 <th>2</th> <th>JC4202</th> <th>parathyroid hormone -</th> <th>1.32e+02</th>	2	JC4202	parathyroid hormone -	1.32e+02
34	36	83.7 <td>116<th>2</th><th>S22553</th><th>ig heavy chain V reg1</th><th>1.32e+02</th></td>	116 <th>2</th> <th>S22553</th> <th>ig heavy chain V reg1</th> <th>1.32e+02</th>	2	S22553	ig heavy chain V reg1	1.32e+02
35	36	83.7 <td>335<th>2</th><th>S35126</th><th>anthranilate phosphor</th><th>1.32e+02</th></td>	335 <th>2</th> <th>S35126</th> <th>anthranilate phosphor</th> <th>1.32e+02</th>	2	S35126	anthranilate phosphor	1.32e+02
36	36	83.7 <td>350<th>2</th><th>B39364</th><th>GDE-1 embryonic growt</th><th>1.32e+02</th></td>	350 <th>2</th> <th>B39364</th> <th>GDE-1 embryonic growt</th> <th>1.32e+02</th>	2	B39364	GDE-1 embryonic growt	1.32e+02
37	36	83.7 <td>366<th>2</th><th>139518</th><th>lipoprotein - Actinob</th><th>1.32e+02</th></td>	366 <th>2</th> <th>139518</th> <th>lipoprotein - Actinob</th> <th>1.32e+02</th>	2	139518	lipoprotein - Actinob	1.32e+02
38	36	83.7 <td>367<th>2</th><th>139649</th><th>regulatory protein Dn</th><th>1.32e+02</th></td>	367 <th>2</th> <th>139649</th> <th>regulatory protein Dn</th> <th>1.32e+02</th>	2	139649	regulatory protein Dn	1.32e+02
39	36	83.7 <td>372<th>2</th><th>D64716</th><th>hypothetical protein</th><th>1.32e+02</th></td>	372 <th>2</th> <th>D64716</th> <th>hypothetical protein</th> <th>1.32e+02</th>	2	D64716	hypothetical protein	1.32e+02
40	36	83.7 <td>381<th>2</th><th>S65212</th><th>hypothetical protein</th><th>1.32e+02</th></td>	381 <th>2</th> <th>S65212</th> <th>hypothetical protein</th> <th>1.32e+02</th>	2	S65212	hypothetical protein	1.32e+02
41	36	83.7 <td>399<th>2</th><th>E33282</th><th>DNA-binding protein (</th><th>1.32e+02</th></td>	399 <th>2</th> <th>E33282</th> <th>DNA-binding protein (</th> <th>1.32e+02</th>	2	E33282	DNA-binding protein (1.32e+02
42	36	83.7 <td>553<th>1</th><th>G1BPSV</th><th>gene 1 protein - spir</th><th>1.32e+02</th></td>	553 <th>1</th> <th>G1BPSV</th> <th>gene 1 protein - spir</th> <th>1.32e+02</th>	1	G1BPSV	gene 1 protein - spir	1.32e+02
43	36	83.7 <td>989<th>2</th><th>156333</th><th>apc1:lipoprotein B - ra</th><th>1.32e+02</th></td>	989 <th>2</th> <th>156333</th> <th>apc1:lipoprotein B - ra</th> <th>1.32e+02</th>	2	156333	apc1:lipoprotein B - ra	1.32e+02
44	36	83.7 <td>1070<th>2</th><th>A54600</th><th>phosphatidylinositol</th><th>1.32e+02</th></td>	1070 <th>2</th> <th>A54600</th> <th>phosphatidylinositol</th> <th>1.32e+02</th>	2	A54600	phosphatidylinositol	1.32e+02
45	36	83.7 <td>1150<th>2</th><th>S49956</th><th>probable membrane pro</th><th>1.32e+02</th></td>	1150 <th>2</th> <th>S49956</th> <th>probable membrane pro</th> <th>1.32e+02</th>	2	S49956	probable membrane pro	1.32e+02

ALIGNMENTS

RESULT 1

ENTRY

1H7H

#type complete

cyclic parathyroid hormone residues 1 34 mutant M8NLE,

TITLE

K13ORX, S17E, M18NLE - synthetic the solution structure of cyclic human parathyroid hormone fragment 1 - 34, NMR, 10 structures

PDB-TITLE

#formal_name synthetic

ORGANISM

A68105

Roesech, P.; Seidel, G.; Schaefer, W.; Esswein, A.; Hofmann, E.

#authors

#submitted to the Brookhaven Protein Data Bank, April 1997

#cross-references

PDB:1H7H Resolution: not applicable

COMMENT

Resolution: not applicable

KEYWORDS

cyclic; human parathyroid hormone; norleucine NMR structure; ornithine

FEATURE

4-6

#region helix (right hand 3-10)\

SUMMARY

20-29

#region helix (right hand alpha)

Query Match

100.0%; Score 43; DB 5; Length 34;

Best Local Similarity

100.0%; Pred. No. 2.97e+00;

Matches

7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB

1 SVSEIQL 7

QY

1 SVSEIQL 7

RESULT 2

12WA

#type complete

ENTRY

HPTH(1-34)

parathyroid hormone (residues 1-34) - human

TITLE

ALTEANAME_NAMES

structure of human parathyroid hormone fragment 1-34, NMR 10

PDB-TITLE

structures

ORGANISM

A67856

#formal_name Homo sapiens #common_name man

REFERENCE

Roesech, P.; Marx, U.C.

submitted to the Brookhaven Protein Data Bank, June 1996

#cross-references

PDB:12WA

REFERENCE

TNO01717

Marx, U.C.

#book

in

Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996

COMMENT

Resolution: not applicable

Determination: NMR

```

KEYWORDS          hormone
FEATURE
6-9              #region helix (right hand alpha)\
19-30            #region helix (right hand alpha)
SUMMARY          #length 34 #molecular-weight 418 #checksum 5629

Query Match      100.0%; Score 43; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.97e+00;
Matches          7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      1 SYSSEQ 7
        |||||
QY      1 SYSSEQ 7

Search completed: Thu Jul 30 10:04:51 1998
Job time : 16 secs.

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MISSED

(TW)

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MPsrch_dp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:03:18 1998; Maspar time 2.05 Seconds
85.496 Million cell updates/sec
Abular output not generated.

Title: >US-08-817-547A-4
Description: (1-7) from US08817547A.pep
Perfect Score: 43
Sequence: 1 SVSEIOL 7

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swlss1

Statistics: Mean 20.233; Variance 16.121; scale 1.255

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	43	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	3.67e-01
2	43	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	3.67e-01
3	41	95.3	115	1	PTHY_RAT PARATHYROID HORMONE PR	1.46e+00
4	41	95.3	896	1	APCE_SYNT4 PHYCOBILISOME 100.5 KD	5.55e+00
5	39	90.7	1827	1	CUTL1_SCHRO CUT1 PROTEIN.	5.55e+00
6	39	90.7	1827	1	CUT1_SCHRO CUT1 PROTEIN.	5.55e+00
7	38	88.4	119	1	PTHY_CHICK PARATHYROID HORMONE PR	1.06e+01
8	38	88.4	4124	1	CAIC_CHICK COLLAGEN ALPHA 1(XII)	1.06e+01
9	37	86.0	407	1	Y090_METJA PUTATIVE PROTEASE MJ00	1.98e+01
10	37	86.0	438	1	PR11_DROME DNA PRIMASE 50 KD SUBU	1.98e+01
11	37	86.0	491	1	NIFD_AZOVI NITROGENASE MOLYBDENUM	1.98e+01
12	37	86.0	605	1	VEI_HPV09 REPLICATION PROTEIN E1	1.98e+01
13	37	86.0	615	1	CA13_CHICK COLLAGEN ALPHA 1(III)	1.98e+01
14	37	86.0	675	1	VP55_YEAST VACUOLAR PROTEIN SORTI	1.98e+01
15	37	86.0	764	1	ICCR_DROME IRREGULAR CHISM C-ROU	1.98e+01
16	37	86.0	1116	1	RPOB_HETCA DNA-DIRECTED RNA POLYM	1.98e+01
17	37	86.0	1132	1	JAK2_RAT TYROSINE-PROTEIN KINAS	1.98e+01
18	37	86.0	1145	1	DPOG_DROME DNA POLYMERASE GAMMA (1.98e+01
19	36	83.7	115	1	PTHY_CANFA PARATHYROID HORMONE PR	3.66e+01
20	36	83.7	282	1	DAAA_STAHA D-ALANINE AMINOTRANSF	3.66e+01
21	36	83.7	335	1	TRPD_LACUA ANTHRANILATE PHOSPHORI	3.66e+01
22	36	83.7	350	1	UOG1_MOUSE HYPOTHETICAL UOG-1 PRO	3.66e+01
23	36	83.7	392	1	HRC2_CHLTR HEAT-INDUCIBLE TRANSCR	3.66e+01

RESULT	ID	PTHY_HUMAN	STANDARD	PTHY	ALIGNMENTS
24	36	83.7	393	1	THIL_RHIME ACETYL-COA ACETYLTRANS
25	36	83.7	537	1	Z029_XENLA OOCYTE ZINC FINGER PRO
26	36	83.7	553	1	VG1_SPV4 CAPSID PROTEIN.
27	36	83.7	832	1	KLPI1_SCHPO KINESIN-LIKE PROTEIN 1
28	36	83.7	857	1	CLPB_ECOLI CLPB PROTEIN (HEAT SHO
29	36	83.7	859	1	YOD3_CAEEL HYPOTHETICAL 96.7 KD P
30	36	83.7	1047	1	YBDE_ECOLI HYPOTHETICAL 114.7 KD
31	36	83.7	1070	1	PI1B_HUMAN PHOSPHATIDYLINOSITOL 3
32	36	83.7	1150	1	YIC6_YEAST HYPOTHETICAL 133.0 KD
33	35	81.4	262	1	FLGG_CAUCR FLAGELLAR BASAL-BODY R
34	35	81.4	303	1	Y367_HAEIN HYPOTHETICAL PROTEIN H
35	35	81.4	314	1	REPE_STANU REPLICATION INITIATION
36	35	81.4	325	1	STK3_ECOLI HYPOTHETICAL LYSYL-TRN
37	35	81.4	464	1	WCAM_ECOLI COLANIC ACID BIOSYNTH
38	35	81.4	500	1	ZIPR_DROME ZIPPER PROTEIN PRECURS
39	35	81.4	679	1	PBP2_STREN PENCILLIN-BINDING PRO
40	35	81.4	760	1	YCE5_YEAST HYPOTHETICAL 87.2 KD P
41	35	81.4	853	1	PXA2_YEAST PEROXISOMAL LONG-CHAIN
42	35	81.4	890	1	YOUN_ECOLI PROBABLE SENSOR PROTEI
43	35	81.4	1036	1	P200_MYCPN INTEGRIN ALPHA-E PRECU
44	35	81.4	1167	1	ITAE_MOUSE RNA POLYMERASE BETA SU
45	35	81.4	2109	1	RRPL_VSVS

[1] SEQUENCE FROM N.A.
RA HENDY G.N., KRONENBERG H.M., POTTS J.T. JR., RICH A.;
PROC. NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).
[2] SEQUENCE FROM N.A.
RA HENDY G.N., POTTS J.T. JR., RICH A., KRONENBERG H.M.;
PROC. NATL. ACAD. SCI. U.S.A. 80:2127-2131(1983).
[3] SEQUENCE OF 26-37.
RA JACOBS J.W., KEMPER B., NIALL H.D., HABENER J.F., POTTS J.T. JR.;
NATURE 249:155-157(1974).
[4] SEQUENCE OF 32-68.
RA NIALL H.D., SAUER R.T., JACOBS J.W., KUTTMANN H.T., SEGRE G.V.,
O'RIORDAN J.L.H., AUBACH G.D., POTTS J.T. JR.;
PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).
[5] SEQUENCE OF 61-83 AND 84-115.
RA KUTTMANN H.T., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.,
POTTS J.T. JR.;
BIOCHEMISTRY 17:5723-5729(1978).
[6] SEQUENCE OF 75-100.
RA KUTTMANN H.T., NIALL H.D., JACOBS J.W., BARLING P.M., HENDY G.N.,
O'RIORDAN J.L.H., POTTS J.T. JR.;
TALMADGE R.V., OWEN M.,
PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM,
(1975).
[7]

WORLDWIDE
(TM)

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MSPrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Jul 30 10:03:43 1998; MasPar time 3.80 Seconds
Molecular output not generated. 77.626 Million cell updates/sec

Title: >US-08-817-547A-4
Description: (1-7) from US08817547A.pep
Perfect Score: 43
Sequence: 1 SVSEIQL 7

Scoring table: PAM 150
Gap 15

Searched: 140542 seqs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptremb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_fodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 19.611; Variance 15.404; scale 1.273

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	41	95.3	896	9	055544	HYPOTHETICAL 100.3 KD	1.43e+00
2	39	90.7	105	10	063473	PARATHYROID HORMONE (F	5.71e+00
3	39	90.7	764	8	P93756	RECEPTOR-LIKE PROTEIN	5.71e+00
4	38	88.4	325	3	016546	C35A11.2 PROTEIN.	1.12e+01
5	38	88.4	459	1	013724	HYPOTHETICAL 51.4 KD P	1.12e+01
6	38	88.4	717	11	041942	HYPOTHETICAL 82.9 KD P	1.12e+01
7	38	88.4	958	8	040554	PMLA-35.	1.12e+01
8	37	86.0	287	12	090794	ALPHA-1 TYPE III COLLA	2.16e+01
9	37	86.0	691	10	035804	JANUS PROTEIN TYROSINE	2.16e+01
10	37	86.0	714	10	P70593	A-KINASE ANCHORING PRO	2.16e+01
11	37	86.0	930	9	053173	MGPS.	2.16e+01
12	37	86.0	1145	3	094906	DNA POLYMERASE GAMMA (2.16e+01
13	37	86.0	1810	3	018038	CODED FOR BY C. ELEGAN	2.16e+01
14	37	86.0	2089	2	014676	KIAA0170 PROTEIN.	2.16e+01
15	37	86.0	3456	11	P89201	POLYPROTEIN.	2.16e+01
16	36	83.7	101	3	015625	(FRAGMENT).	4.10e+01
17	36	83.7	189	3	019478	FL15B9.1.	4.10e+01
18	36	83.7	203	1	003401	HYPOTHETICAL 23.4 KD P	4.10e+01
19	36	83.7	356	9	031461	YBGE PROTEIN.	4.10e+01
20	36	83.7	366	9	044163	LIPOPROTEIN PRECURSOR.	4.10e+01

RESULT	ID	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	055544	95.3	896	9	055544	HYPOTHETICAL 100.3 KD	1.43e+00	
2	053544	90.7	105	10	063473	PARATHYROID HORMONE (F	5.71e+00	
3	053544	90.7	764	8	P93756	RECEPTOR-LIKE PROTEIN	5.71e+00	
4	053544	88.4	325	3	016546	C35A11.2 PROTEIN.	1.12e+01	
5	053544	88.4	459	1	013724	HYPOTHETICAL 51.4 KD P	1.12e+01	
6	053544	88.4	717	11	041942	HYPOTHETICAL 82.9 KD P	1.12e+01	
7	053544	88.4	958	8	040554	PMLA-35.	1.12e+01	
8	053544	86.0	287	12	090794	ALPHA-1 TYPE III COLLA	2.16e+01	
9	053544	86.0	691	10	035804	JANUS PROTEIN TYROSINE	2.16e+01	
10	053544	86.0	714	10	P70593	A-KINASE ANCHORING PRO	2.16e+01	
11	053544	86.0	930	9	053173	MGPS.	2.16e+01	
12	053544	86.0	1145	3	094906	DNA POLYMERASE GAMMA (2.16e+01	
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14	053544	86.0	2089	2	014676	KIAA0170 PROTEIN.	2.16e+01	
15	053544	86.0	3456	11	P89201	POLYPROTEIN.	2.16e+01	
16	053544	83.7	101	3	015625	(FRAGMENT).	4.10e+01	
17	053544	83.7	189	3	019478	FL15B9.1.	4.10e+01	
18	053544	83.7	203	1	003401	HYPOTHETICAL 23.4 KD P	4.10e+01	
19	053544	83.7	356	9	031461	YBGE PROTEIN.	4.10e+01	
20	053544	83.7	366	9	044163	LIPOPROTEIN PRECURSOR.	4.10e+01	

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	055544	95.3	896	9	055544	HYPOTHETICAL 100.3 KD	1.43e+00	
2	053544	90.7	105	10	063473	PARATHYROID HORMONE (F	5.71e+00	
3	053544	90.7	764	8	P93756	RECEPTOR-LIKE PROTEIN	5.71e+00	
4	053544	88.4	325	3	016546	C35A11.2 PROTEIN.	1.12e+01	
5	053544	88.4	459	1	013724	HYPOTHETICAL 51.4 KD P	1.12e+01	
6	053544	88.4	717	11	041942	HYPOTHETICAL 82.9 KD P	1.12e+01	
7	053544	88.4	958	8	040554	PMLA-35.	1.12e+01	
8	053544	86.0	287	12	090794	ALPHA-1 TYPE III COLLA	2.16e+01	
9	053544	86.0	691	10	035804	JANUS PROTEIN TYROSINE	2.16e+01	
10	053544	86.0	714	10	P70593	A-KINASE ANCHORING PRO	2.16e+01	
11	053544	86.0	930	9	053173	MGPS.	2.16e+01	
12	053544	86.0	1145	3	094906	DNA POLYMERASE GAMMA (2.16e+01	
13	053544	86.0	1810	3	018038	CODED FOR BY C. ELEGAN	2.16e+01	
14	053544	86.0	2089	2	014676	KIAA0170 PROTEIN.	2.16e+01	
15	053544	86.0	3456	11	P89201	POLYPROTEIN.	2.16e+01	
16	053544	83.7	101	3	015625	(FRAGMENT).	4.10e+01	
17	053544	83.7	189	3	019478	FL15B9.1.	4.10e+01	
18	053544	83.7	203	1	003401	HYPOTHETICAL 23.4 KD P	4.10e+01	
19	053544	83.7	356	9	031461	YBGE PROTEIN.	4.10e+01	
20	053544	83.7	366	9	044163	LIPOPROTEIN PRECURSOR.	4.10e+01	

Thu Jul 30 13:38:18 1998

US-08-817-547A-4.rsp

Page 2

RC	TISSUE-THYROID, AND PARATHYROID;	
RA	SCHMEZLER H.J., GROSS G., MAER H.;	
RL	ADV. GENE TECHNOL. 21:228-229(1984).	
DR	ENML; M54875; G601933; -	
FT	NUMBER	1
SO	SEQUENCE	105 AA; 11746 MW; 6AC3163E CRC32;

Search completed: Thu Jul 30 10:04:16 1998
Job time : 33 secs.

WATERMAN
(TM)

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MsrchLpp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:07:26 1998; MasPar time 2.53 Seconds
Molecular output not generated. 36.409 Million cell updates/sec

Title: >US-08-817-547A-5
Description: (1-6) from US08817547A.pep
Perfect Score: 35
Sequence: 1 SVSEIQ 6

Scoring table:
GAP 15
PAM 150

Searched: 124785 seqs, 15338987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseg31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 12.234; Variance 31.551; scale 0.388
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	35	100.0	16 25	W21948	Fusion protein compri	2.24e+02
2	35	100.0	20 25	W21947	Fusion protein compri	2.24e+02
3	35	100.0	33 3	P82176	Sequence of parathyro	2.24e+02
4	35	100.0	34 4	R22293	Human parathyroid hor	2.24e+02
5	35	100.0	34 22	W19994	Cyclised human parath	2.24e+02
6	35	100.0	34 22	W17962	Human PTH analogue [C	2.24e+02
7	35	100.0	34 22	W17961	Human PTH analogue [C	2.24e+02
8	35	100.0	34 22	W17960	Human PTH analogue [C	2.24e+02
9	35	100.0	34 8	R41561	[Lys16, Glu27]hPTH (1	2.24e+02
10	35	100.0	34 9	R58054	[Lys16, Glu18, A19, R22, T	2.24e+02
11	35	100.0	34 9	R58193	[Lys16, Glu18, A19, R22, T	2.24e+02
12	35	100.0	34 3	P50517	Sequence of methionin	2.24e+02
13	35	100.0	34 8	R41549	ID-Ser3]hPTH (1-34)NH	2.24e+02
14	35	100.0	34 8	R41551	[Thr16]hPTH (1-34)NH	2.24e+02
15	35	100.0	34 9	R58232	[Lys32]hPTH (1-34)NH	2.24e+02
16	35	100.0	34 22	W17966	Human PTH analogue [C	2.24e+02
17	35	100.0	34 22	W17939	Human parathyroid hor	2.24e+02
18	35	100.0	34 22	W17951	Human parathyroid hor	2.24e+02
19	35	100.0	35 14	R74504	Parathyroid hormone p	2.24e+02

20	35	100.0	35 14	R74503	Parathyroid hormone p	2.24e+02
21	35	100.0	35 14	R74510	Parathyroid hormone p	2.24e+02
22	35	100.0	35 14	R74418	Parathyroid hormone p	2.24e+02
23	35	100.0	35 14	R74417	Parathyroid hormone p	2.24e+02
24	35	100.0	36 9	R58200	[D-His9]-hPTH(1-36)-NH	2.24e+02
25	35	100.0	36 9	R58045	[Lys16, Glu18, A19, R22, T	2.24e+02
26	35	100.0	36 9	R58055	[Lys16, Glu18, A19, R22, T	2.24e+02
27	35	100.0	36 9	R58238	[D-Ser30]-hPTH(1-36)-NH	2.24e+02
28	35	100.0	36 9	R58213	[D-Ser17]-hPTH(1-36)-NH	2.24e+02
29	35	100.0	36 9	R58214	[Ala13]-hPTH(1-38)-OH	2.24e+02
30	35	100.0	38 9	R58103	[Ala13]-hPTH(1-38)-OH	2.24e+02
31	35	100.0	38 9	R58147	[Leu21]-hPTH(1-38)-OH	2.24e+02
32	35	100.0	38 9	R58157	[Arg27]-hPTH(1-38)-OH	2.24e+02
33	35	100.0	38 9	R58115	[Lys16]-hPTH(1-38)-OH	2.24e+02
34	35	100.0	38 9	R58116	[Lys16]-hPTH(1-38)-OH	2.24e+02
35	35	100.0	38 10	R54234	[Ser16]-hPTH(1-38)-OH	2.24e+02
36	35	100.0	44 26	P30015	PTH N-terminal.	2.24e+02
37	35	100.0	47 25	W21945	Human parathyroid hor	2.24e+02
38	35	100.0	84 27	W25687	Fusion protein compri	2.24e+02
39	35	100.0	84 5	R29563	Human parathyroid hor	2.24e+02
40	35	100.0	84 5	R29565	Oxidation resistant p	2.24e+02
41	35	100.0	84 5	R29565	Oxidation resistant [2.24e+02
42	35	100.0	84 25	W29420	Human parathyroid hor	2.24e+02
43	35	100.0	84 5	R28846	Oxidation resistant [2.24e+02
44	35	100.0	84 4	R23378	Bovine parathyroid ho	2.24e+02
45	35	100.0	102 4	P40252	Stability-enhanced hu	2.24e+02

ALIGNMENTS

RESULT	ID	Accession	Length	Score	Location/Qualifiers
1	W21948	standard; Protein; 16 AA.	16	102	
2	W21948	30-JAN-1998 (first entry)	16	102	
3	W21948	Fusion protein comprising linker and PTH 1-37 (residues 1-7).	16	102	
4	W21948	Linker: parathyroid hormone 1-37; PTH 1-37; streptavidin.	16	102	
5	W21948	Fusion protein; recombinant production; TEV Nta protease;	16	102	
6	W21948	tobacco etch virus.	16	102	
7	W21948	Synthetic.	16	102	
8	W21948	OS Homo sapiens.	16	102	
9	W21948	Key	16	102	
10	W21948	Peptide	16	102	
11	W21948	Peptide	16	102	
12	W21948	Peptide	16	102	
13	W21948	Peptide	16	102	
14	W21948	Peptide	16	102	
15	W21948	Peptide	16	102	
16	W21948	Peptide	16	102	
17	W21948	Peptide	16	102	
18	W21948	Peptide	16	102	
19	W21948	Peptide	16	102	
20	W21948	Peptide	16	102	
21	W21948	Peptide	16	102	
22	W21948	Peptide	16	102	
23	W21948	Peptide	16	102	
24	W21948	Peptide	16	102	
25	W21948	Peptide	16	102	
26	W21948	Peptide	16	102	
27	W21948	Peptide	16	102	
28	W21948	Peptide	16	102	
29	W21948	Peptide	16	102	
30	W21948	Peptide	16	102	
31	W21948	Peptide	16	102	
32	W21948	Peptide	16	102	
33	W21948	Peptide	16	102	
34	W21948	Peptide	16	102	
35	W21948	Peptide	16	102	
36	W21948	Peptide	16	102	
37	W21948	Peptide	16	102	
38	W21948	Peptide	16	102	
39	W21948	Peptide	16	102	
40	W21948	Peptide	16	102	
41	W21948	Peptide	16	102	
42	W21948	Peptide	16	102	
43	W21948	Peptide	16	102	
44	W21948	Peptide	16	102	
45	W21948	Peptide	16	102	

CC removal on an iminobiotin column followed by chromatography on a
 CC fractogel and reverse phase HPLC.
 SQ Sequence 16 AA;

Query Match 100.0%; Score 35; DB 25; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.24e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 svseiq 15
 |||||
 QY 1 svseiq 6

RESULT 2

ID W21947 standard; Protein; 20 AA.

AC W21947;

DT 30-JAN-1998 (first entry)

DE Fusion protein comprising linker and PTH 1-37 (residues 1-7).
 Linker; parathyroid hormone 1-37; PTH 1-37; streptavidin;
 fusion protein; recombinant production; thrombin.
 Synthetic.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..1

FT Peptide /note= "Met(13-139) streptavidin residue"

FT Peptide 2..13

FT Peptide /note= "linker cleavable by thrombin"

FT Peptide 14..20

FT Peptide /note= "parathyroid hormone 1-37 (residues 1-7)"

PN W09718314-A1.

PD 22-MAY-1997.

PF 06-NOV-1996; E04850.

PR 16-NOV-1995; DE-042702.

PA (BOE) BOEHRINGER MANNHEIM GMBH.

PI Kopetzki E;

PI WPI; 97-289290/26.

DR N-PSDB: T73911.

PT Recombinant production of peptide(s) as fusions with streptavidin
 attached via cleavable linker - especially for utrotropin and
 parathyroid hormone production

PS Example 3; Fig 3; 37pp; German.

CC The DNA encoding the present sequence, a linker and residues 1-7 of
 the parathyroid hormone 1-37 (PTH 1-37) peptide with codon usage
 optimised for E. coli, was ligated to the 2.9 kb NheI-HindIII

CC fragment of pSAM-CORE, which contains the Met(13-139) streptavidin
 (SA) sequence, to give pSA-THRO-PTH. pSA-THRO-PTH and the lacIq

CC repressor plasmid PUBS500 were used to transform E. coli K12 RM82.
 The transformants were grown, with IPTG induction, in medium

CC containing kanamycin and ampicillin. Cells were harvested, lysed
 and isolated inclusion bodies solubilised in guanidine

CC hydrochloride, and renatured by dilution in pH 7 phosphate buffer.
 The solution was clarified and the supernatant concentrated and

CC purified on a column of immobilised iminobiotin. The purified
 material was incubated with thrombin and the PTH 1-37 fragment

CC released, recovered by SA fragment removal on an iminobiotin
 column followed by chromatography on a fractogel and reverse phase

CC HPLC.

CC

CC

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Search completed: Thu Jul 30 10:07:41 1998
 Job time : 15 secs.

MORSE

(TM)

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Masrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:06:50 1998; MasPar time 3.00 Seconds
Molecular output not generated. 73.160 Million cell updates/sec

Title: >US-08-817-547A-5
Description: (1-6) from US08817547A.pep
Perfect Score: 35
Sequence: 1 SVSEIQ 6

Scoring table: PAM 150
Gap 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plf56
1:plf1 2:plf2 3:plf3 4:plf4 5:nrl3d

Statistics: Mean 17.547; Variance 15.799; scale 1.111

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	35	100.0	34	5	1H7H cyclic parathyroid ho	2.66e+01
2	35	100.0	34	5	1ZWA parathyroid hormone (2.66e+01
3	35	100.0	37	5	1HPH parathyroid hormone f	2.66e+01
4	35	100.0	115	2	JC4202 parathyroid hormone -	2.66e+01
5	35	100.0	115	1	PTNU parathyroid hormone p	2.66e+01
6	35	100.0	115	1	PTPG parathyroid hormone p	2.66e+01
7	35	100.0	303	2	A64150 hypothetical protein	2.66e+01
8	35	100.0	853	2	S34682 probable transport pr	2.66e+01
9	35	100.0	1116	2	S41915 DNA-directed RNA poly	2.66e+01
10	33	94.3	37	5	1ZWC parathyroid hormone (8.67e+01
11	33	94.3	115	2	PTBO parathyroid hormone p	8.67e+01
12	33	94.3	115	2	A05091 parathyroid hormone p	8.67e+01
13	33	94.3	315	2	E69400 3-hydroxycyl-COA deh	8.67e+01
14	33	94.3	424	2	I39310 zinc finger protein 2	8.67e+01
15	33	94.3	428	2	A42311 A-kinase anchor prote	8.67e+01
16	33	94.3	540	2	S35071 auxin-resistance prot	8.67e+01
17	33	94.3	801	2	PC6010 RNA helicase Gu - hum	8.67e+01
18	33	94.3	896	2	S59990 phycobillosome anchor	8.67e+01
19	33	94.3	896	2	S76064 hypothetical protein	8.67e+01
20	32	91.4	270	2	B32835 hypothetical ntra pro	1.53e+02
21	32	91.4	329	2	G69210 conserved hypothetical	1.53e+02
22	32	91.4	422	2	A34589 lin-10 protein - Caen	1.53e+02
23	32	91.4	507	2	B69957 conserved hypothetical	1.53e+02

24	32	91.4	537	2	S50344 aspergillopepsin homo	1.53e+02
25	32	91.4	697	2	G70133 flagellar biosynthet	1.53e+02
26	31	88.6	109	5	1VTG epsilon thrombin (EC	2.66e+02
27	31	88.6	109	5	1UCYE thrombin (EC 3.4.21.5	2.66e+02
28	31	88.6	146	2	S76533 hypothetical protein	2.66e+02
29	31	88.6	259	5	1TRBOH thrombin (EC 3.4.21.5	2.66e+02
30	31	88.6	259	5	1TRBK thrombin (EC 3.4.21.5	2.66e+02
31	31	88.6	259	5	1IBRK thrombin (EC 3.4.21.5	2.66e+02
32	31	88.6	259	5	1UCYK thrombin (EC 3.4.21.5	2.66e+02
33	31	88.6	259	5	1UCYK thrombin (EC 3.4.21.5	2.66e+02
34	31	88.6	259	5	1VTTH alpha thrombin (EC 3.	2.66e+02
35	31	88.6	259	5	1TROCH thrombin (EC 3.4.21.5	2.66e+02
36	31	88.6	298	2	S76437 hypothetical protein	2.66e+02
37	31	88.6	392	2	A69474 myo-inositol-1-phosph	2.66e+02
38	31	88.6	402	2	S47329 Oxa1 protein precursor	2.66e+02
39	31	88.6	415	2	S63221 DNA-directed RNA poly	2.66e+02
40	31	88.6	416	2	C47017 probable transcriptio	2.66e+02
41	31	88.6	635	2	S19011 endo-1,4-beta-xylanas	2.66e+02
42	31	88.6	677	2	S33664 flagella-associated p	2.66e+02
43	31	88.6	994	2	A47474 MADP-ADP-ribosyltrans	2.66e+02
44	31	88.6	1039	2	S02711 cellulase (EC 3.2.1.4	2.66e+02
45	31	88.6	3066	1	JQ1662 genome polyprotein -	2.66e+02

ALIGNMENTS

RESULT	1	1H7H	#type complete
ENTRY		cyclic parathyroid hormone residues 1 34 mutant M8NLE,	
TITLE		K130RN, S17E, M18NLE - synthetic	
PDB_TITLE		the solution structure of cyclic human parathyroid hormone	
ORGANISM		fragment 1 - 34, NMR, 10 structures	
REFERENCE		#formal_name synthetic	
authors		A68105	
#authors		Roesch, P.; Seidel, G.; Schaefer, W.; Esswein, A.; Hofmann,	
E.			
#submission		submitted to the Brookhaven Protein Data Bank, April 1997	
#cross-references		PDB:1H7H	
COMMENT		Resolution: not applicable	
COMMENT		Determination: NMR	
KEYWORDS		cyclic; human parathyroid hormone; norleucine NMR structure;	
ornithine			
FEATURE			
4-6		#region helix (right hand 3-10) \	
20-29		#region helix (right hand alpha)	
SUMMARY		#length 34 #molecular-weight 4146 #checksum 5768	
Query Match		100.0%; Score 35; DB 5; Length 34;	
Best Local Similarity 100.0%; Pred. No. 2.66e+01;			
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Db	1	SVSEIQ 6	
Oy	1	SVSEIQ 6	
RESULT	2	1ZWA	#type complete
ENTRY		parathyroid hormone (residues 1-34) - human	
TITLE		HP7H(1-34)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 1-34, NMR 10	
PDB_TITLE			
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67856	
authors		Roesch, P.; Marx, U.C.	
#authors		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:1ZWA	
REFERENCE		TN001717	
authors		Marx, U.C.	
#book			
COMMENT		in Strukturen Verschiedener Parathormonfragmente in Loessung,	
COMMENT		pp.0, Bayreuth : University of Bayreuth (Thesis), 1996	
COMMENT		Resolution: not applicable	
COMMENT		Determination: NMR	

KEYWORDS hormone
 FEATURE
 6-9 #region helix (right hand alpha) \
 19-30 #region helix (right hand alpha) \
 SUMMARY #length 34 #molecular-weight 4118 #checksum 5629
 Query Match 100.0%; Score 35; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.66e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 SVSEIQ 6
 QY 1 SVSEIQ 6

Search completed: Thu Jul 30 10:07:08 1998
 Job time : 18 secs.


```

RESULT 2
ID PTH_CANFA STANDARD: PRT: 115 AA.
AC P52212;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.
OS CANIS FAMILIARIS (DOG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.
CC EUHERIA; CARNIVORA.
[1]
RN
RP SEQUENCE FROM N.A.
RC TISSUE-PARATHYROID.
RX MEDLINE: 95369696.
RA ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,
RA DEMILLE J.W., CAPEN C.C.;
RA GENE 160:241-243(1995).
-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
      BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL: U15662; G558916; -
DR PROSITE: PS00335; PARATHYROID; 1.
KM HORMONE; SIGNAL.
FT SIGNAL 1 25 BY SIMILARITY.
FT PROPEP 26 31 BY SIMILARITY.
FT CHAIN 32 115 PARATHYROID HORMONE.
SQ SEQUENCE 115 AA; 12957 MW; 16ED0BEC CRC32;

Query Match 100.0%; Score 35; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 5.84e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 32 SVSEIQ 37
QY 1 SVSEIQ 6

```

Search completed: Thu Jul 30 10:05:51 1998
 Job time : 7 secs.

W O R L D
(TM)

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Msrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:06:08 1998; Maspar time 3.81 Seconds
Abular output not generated. 66.309 Million cell updates/sec

Title: >US-08-817-547A-5
Description: (1-6) from US0817547A.pep
Perfect Score: 35
Sequence: 1 SVSEIQ 6

Scoring table: PAM 150
Gap 15

Searched: 140542 seqs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptemb15
1:sp_fungi1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 17.730; Variance 12.970; scale 1.367

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	35	100.0	714	10	P70593	A-KINASE ANCHORING PRO	8.71e+00
2	35	100.0	771	3	Q20026	CODED FOR BY C. ELEGAN	8.71e+00
3	33	94.3	315	9	Q29062	3-HYDROXYACYL-CoA DEHY	3.59e+01
4	33	94.3	324	9	Q07213	HYPOHETICAL 35.5 KD P	3.59e+01
5	33	94.3	424	2	Q15916	ZID, ZINC FINGER PROTE	3.59e+01
6	33	94.3	484	2	Q18032	TOSF1A.4.	3.59e+01
7	33	94.3	794	4	Q18742	LU-BEAM-1.	3.59e+01
8	33	94.3	801	2	Q13436	NUCLEOLAR RNA HELICASE	3.59e+01
9	33	94.3	820	4	Q18743	LU-BEAM-1.	3.59e+01
10	33	94.3	896	9	Q55544	HYPOHETICAL 100.3 KD	3.59e+01
11	33	94.3	905	4	Q18741	LU-BEAM-1.	3.59e+01
12	33	94.3	1967	11	Q10378	LARGE PROTEIN.	3.59e+01
13	32	91.4	43	2	Q14359	GALACTOSE-1-PHOSPHATE	7.10e+01
14	32	91.4	91	9	P72152	FLAG.	7.10e+01
15	32	91.4	131	11	P87572	E4 ORF1.	7.10e+01
16	32	91.4	239	9	P74971	PV. VESICATORIA ORF1.	7.10e+01
17	32	91.4	258	9	Q52785	ABC-TYPE PERMEASE HOMO	7.10e+01
18	32	91.4	270	9	Q53342	ORE 5' OF RON.	7.10e+01
19	32	91.4	317	11	Q66606	VIRAL NUCLEOPROTEIN.	7.10e+01
20	32	91.4	329	9	Q26918	CONSERVED PROTEIN.	7.10e+01

21	32	91.4	466	2	Q13283	GAP SH3 BINDING PROTEI	7.10e+01
22	32	91.4	595	1	Q14301	BETA-TRANSDUCIN.	7.10e+01
23	32	91.4	673	9	Q44759	FLHA.	7.10e+01
24	32	91.4	679	8	Q39603	HEAT SHOCK PROTEIN 70B	7.10e+01
25	32	91.4	697	9	Q44909	FLAGELLAR EXPORT PROTE	7.10e+01
26	31	88.6	105	10	Q63473	PARATHYROID HORMONE (F	1.37e+02
27	31	88.6	146	9	Q53737	HYPOHETICAL 16.4 KD P	1.37e+02
28	31	88.6	251	3	Q26980	ZEN TC (FRAGMENT).	1.37e+02
29	31	88.6	265	9	Q07802	HYPOHETICAL 27.4 KD P	1.37e+02
30	31	88.6	292	2	Q14538	MACROPHAGE LECTIN 2.	1.37e+02
31	31	88.6	298	9	P74465	PLIN BIOGENESIS PROTE	1.37e+02
32	31	88.6	311	9	P71859	HYPOHETICAL 33.9 KD P	1.37e+02
33	31	88.6	316	9	Q47701	POLYSACCHARIDE CHAIN L	1.37e+02
34	31	88.6	444	9	Q51919	PUTATIVE CHAPERONIN (1.37e+02
35	31	88.6	465	10	P97855	RAS-GTPASE-ACTIVATING	1.37e+02
36	31	88.6	471	4	P79386	ORPHAN NUCLEAR RECEPT	1.37e+02
37	31	88.6	625	10	Q61468	MEGAROCYTE POTENTIA	1.37e+02
38	31	88.6	764	8	P93756	RECEPTOR-LIKE PROTEIN	1.37e+02
39	31	88.6	815	8	Q22113	HCR2.	1.37e+02
40	31	88.6	939	1	Q06078	SIMILAR TO TRANSCRIPTI	1.37e+02
41	31	88.6	1026	11	Q36363	DNA POLYMERASE (EC 2.7	1.37e+02
42	31	88.6	1106	2	Q15034	KIA0318 (FRAGMENT).	1.37e+02
43	31	88.6	1144	3	P91304	CODED FOR BY C. ELEGAN	1.37e+02
44	31	88.6	1277	12	Q98902	NEURL CELL ADHESION M	1.37e+02
45	31	88.6	1819	3	Q16625	K106.3 PROTEIN.	1.37e+02

ALIGNMENTS

RESULT 1
ID P70593 PRELIMINARY: PRT: 714 AA.
AC P70593:
DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
DI 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DR 01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
DE A-KINASE ANCHORING PROTEIN AKAP150.
OS RATTUS NORVEGICUS (RAT)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
RN [1]
RP SEQUENCE FROM N.A.
RA TAKAI Y., IRIE M., TOYODA A., HATA Y.;
RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U67136; G1532182; -
SQ SEQUENCE 714 AA; 75938 MW; 0A1CF1F CRC32;

Query Match 100.0%; Score 35; DB 10; Length 714;
Best Local Similarity 100.0%; Pred. No. 8.71e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB	4	SVSEIQ 9
QY	1	SVSEIQ 6
RESULT 2		
AC	Q20026	PRELIMINARY: PRT: 771 AA.
DI	01-NOV-1996 (TREMBLREL. 01, CREATED)	
DR	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)	
DE	01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)	
DE	CODED FOR BY C. ELEGANS CDNA CEESB82F.	
GN	F5C8.7.	
OS	CAENORHABDITIS ELEGANS.	
OC	EUKARYOTA; METAZOA; ACLOMATES; NEMATODA; SECCERNTEA; RHABDITIDA.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE: 94150718.	
RA	WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,	
RA	BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,	
RA	CRATON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,	
RA	GARNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSON L.,	
RA	JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,	

RA LIGHTNING J., LLOYD C., MCGRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SWALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
 RL NATURE 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA WD X;
 RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA WATERSTON R.;
 RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; U00941; G1072187; -;
 SQ SEQUENCE 771 AA; 87311 MW; 5AE2EE3F CRC32;

Query Match 100.0%; Score 35; DB 3; Length 771;
 Best Local Similarity 100.0%; Pred. No. 8.71e+00;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 190 SYSEIO 195
 |||||
 QY 1 SYSEIO 6

Search completed: Thu Jul 30 10:06:33 1998
 Job time : 25 secs.

CC removal on an iminobiotin column followed by chromatography on a
 CC fractogel and reverse phase HPLC.
 SQ Sequence 16 AA;

Query Match 100.0%; Score 28; DB 25; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7.96e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 10 svsel 14
 11111
 QY 1 SVSEI 5

RESULT 2

ID W21947 standard; Protein; 20 AA.
 AC W21947;
 DT 30-JAN-1998 (first entry)
 DE Fusion protein comprising linker and PTH 1-37 (residues 1-7).
 Linker: parathyroid hormone 1-37; PTH 1-37; streptavidin;
 fusion protein; recombinant production; thrombin.
 Synthetic.
 US Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..1 /note= "Met(13-139) streptavidin residue"
 FT Peptide 2..13 /note= "linker cleavable by thrombin"
 FT Peptide 14..20 /note= "parathyroid hormone 1-37 (residues 1-7)"
 FT Peptide
 PN W09718314-A1.
 PD 22-MAY-1997.
 PE 06-NOV-1996; E04850.
 PR 16-NOV-1995; DE-042702.
 PA (BOEP) BOEHRINGER MANNHEIM GMBH.
 PI Kopeckzi E;
 DR WPI: 97-289290/26.
 DR N-PSDB; T73911.
 PT Recombinant production of peptide(s) as fusions with streptavidin
 attached via cleavable linker - especially for utrotropin and
 parathyroid hormone production
 PT parathyroid hormone production
 PS Example 3: Fig 3; 37pp; German.
 CC The DNA encoding the present sequence, a linker and residues 1-7 of
 the parathyroid hormone 1-37 (PTH 1-37) peptide with codon usage
 optimised for E. coli, was ligated to the 2.9 kb NheI-HindIII
 fragment of PSAM-CORE, which contains the Met(13-139) streptavidin
 (SA) sequence. to give PSA-THRO-PTH. PSA-THRO-PTH and the lacIq
 repressor plasmid pBS500 were used to transform E. coli K12 RM82.
 The transformants were grown, with IPTG induction, in medium
 containing kanamycin and ampicillin. Cells were harvested, lysed
 and isolated inclusion bodies solubilised in guanidine
 hydrochloride, and renatured by dilution in pH 7 phosphate buffer.
 CC The solution was clarified and the supernatant concentrated and
 purified on a column of immobilised iminobiotin. The purified
 material was incubated with thrombin and the PTH 1-37 fragment
 released recovered by SA fragment removal on an iminobiotin
 column followed by chromatography on a fractogel and reverse phase
 HPLC.
 CC
 SQ Sequence 20 AA;

Query Match 100.0%; Score 28; DB 25; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.96e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 14 svsel 18
 11111
 QY 1 SVSEI 5

Search completed: Thu Jul 30 10:09:58 1998
 Job time : 16 secs.

WIRE (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:09:06 1998; Maspar time 2.97 Seconds
61.602 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-6
Description: (1-5) from US08817547A.pep
Perfect Score: 28
Sequence: 1 SVSET 5

Scoring table: PAM 150
Gap 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr56
1:pir1 2:pir2 3:pir3 4:pir4 5:nr13d

Statistics: Mean 16.244; Variance 13.192; scale 1.231

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	28	100.0	34	5 1H7H	cyclic parathyroid ho	3.60e+02
2	28	100.0	34	5 1ZWA	parathyroid hormone (3.60e+02
3	28	100.0	37	5 1HPH	parathyroid hormone f	3.60e+02
4	28	100.0	115	2 JCA202	parathyroid hormone -	3.60e+02
5	28	100.0	126	2 S75413	hypothetical protein	3.60e+02
6	28	100.0	227	2 S54466	hypothetical protein	3.60e+02
7	28	100.0	303	2 A64150	glutathione synthase	3.60e+02
8	28	100.0	308	2 JQ1401	transaldolase b (EC 2	3.60e+02
9	28	100.0	316	5 1ONRA	transaldolase b (EC 2	3.60e+02
10	28	100.0	316	5 1ONRB	transaldolase b (EC 2	3.60e+02
11	28	100.0	316	5 1UCWB	transaldolase (EC 2.2	3.60e+02
12	28	100.0	316	5 1UCWB	transaldolase (EC 2.2	3.60e+02
13	28	100.0	344	2 A30544	dnak-type molecular c	3.60e+02
14	28	100.0	362	2 S12895	polygalacturonase (EC	3.60e+02
15	28	100.0	387	2 S33517	tubulin alpha chain -	3.60e+02
16	28	100.0	389	2 S20933	naringenin-chalcone s	3.60e+02
17	28	100.0	389	2 S33610	naringenin-chalcone s	3.60e+02
18	28	100.0	389	2 S35167	naringenin-chalcone s	3.60e+02
19	28	100.0	389	2 S26144	naringenin-chalcone s	3.60e+02
20	28	100.0	405	2 A35620	coenzyme F420 hydroge	3.60e+02
21	28	100.0	408	2 A69040	coenzyme F420-reducin	3.60e+02
22	28	100.0	415	2 S63221	DNA-directed RNA poly	3.60e+02
23	28	100.0	420	2 C64552	exonuclease VII, latg	3.60e+02

24	28	100.0	450	2 A45547	tubulin alpha-II chain	3.60e+02
25	28	100.0	451	2 JCA133	alpha-tubulin isoform	3.60e+02
26	28	100.0	453	2 S07459	tubulin alpha-I chain	3.60e+02
27	28	100.0	458	2 S44741	C02C2.3 protein - Cae	3.60e+02
28	28	100.0	491	2 B69499	sodium- and chloride-	3.60e+02
29	28	100.0	609	2 S55957	hypothetical protein	3.60e+02
30	28	100.0	609	2 S28698	dnak-type molecular c	3.60e+02
31	28	100.0	628	2 A69381	type II secretion sys	3.60e+02
32	28	100.0	691	2 S54262	methyl-accepting chem	3.60e+02
33	28	100.0	737	2 S63453	probable RNA helicase	3.60e+02
34	28	100.0	741	2 S50340	CHL12 protein - yeast	3.60e+02
35	28	100.0	853	2 S34682	cellulase transport pr	3.60e+02
36	28	100.0	915	2 A43802	cellulase (EC 3.2.1.4	3.60e+02
37	28	100.0	921	2 A55854	seca protein - Caulob	3.60e+02
38	28	100.0	962	2 S58107	hypothetical protein	3.60e+02
39	28	100.0	974	2 A44484	transcription regulat	3.60e+02
40	28	100.0	1039	2 S02711	cellulase (EC 3.2.1.4	3.60e+02
41	28	100.0	1116	2 S41915	DNA-directed RNA poly	3.60e+02
42	28	100.0	1146	2 S07915	RF2 protein - yeast (3.60e+02
43	28	100.0	1232	2 B39432	ATP-dependent deoxyri	3.60e+02
44	28	100.0	1332	2 B39434	homeotic protein CDP	3.60e+02
45	28	100.0	2844	2 S28291	hypothetical protein	3.60e+02

ALIGNMENTS

RESULT 1
ENTRY 1H7H #type complete
TITLE cyclic parathyroid hormone residues 1-34 mutant M8NLE,
K130RN, S17E, M18NLE - synthetic
PDB-TITLE the solution structure of cyclic human parathyroid hormone
fragment 1 - 34, NMR, 10 structures
ORGANISM #formal_name synthetic
REFERENCE A68105
#authors Roesch, P.; Seidel, G.; Schaefer, W.; Esswein, A.; Hofmann, E.
#submission submitted to the Brookhaven Protein Data Bank, April 1997
COMMENT #cross-References PDB:1H7H
COMMENT Resolution: not applicable
COMMENT Determination: NMR
KEYWORDS cyclic; human parathyroid hormone; norleucine NMR structure;
ornithine
FEATURE
4-6 #region helix (right hand 3-10)\
20-29 #region helix (right hand alpha)
SUMMARY #length 34 #molecular-weight 4146 #checksum 5768
Query Match 100.0%; Score 28; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.60e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 SVSET 5
Qy 1 SVSET 5
RESULT 2
ENTRY 1ZWA #type complete
TITLE parathyroid hormone (residues 1-34) - human
ALTERNATE_NAMES HPTH(1-34)
PDB-TITLE structure of human parathyroid hormone fragment 1-34, NMR 10
structures
ORGANISM #formal_name Homo sapiens #common_name man
REFERENCE A67856
#authors Roesch, P.; Marx, U.C.
#submission submitted to the Brookhaven Protein Data Bank, June 1996
REFERENCE TN001717
#cross-References PDB:1ZWA
#authors Marx, U.C.
#book in Struktur und Verschiedener Parathormonfragmente in Loesung,
pp.0, Bayreuth : Universitaet of Bayreuth (Thesis), 1996
COMMENT Resolution: not applicable
COMMENT Determination: NMR

KEYWORDS hormone
FEATURE
6-9 #region helix (right hand alpha) \
19-30 #region helix (right hand alpha)
SUMMARY #length 34 #molecular-weight 418 #checksum 5629
Query Match 100.0%; Score 28; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.60e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 SVSEI 5
|||
QY 1 SVSEI 5

Search completed: Thu Jul 30 10:09:24 1998
Job time : 18 secs.

OS CANIS FAMILIARIS (DOG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; CARNIVORA.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE-PARATHYROID;
 RX MEDLINE; 95369696.
 RA ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,
 RA DEWILLE J.W., CAPEN C.C.;
 RL GENE 160:241-243(1995).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 DR EMBL; U15662; G558916; -.
 DR PROSITE; PS00335; PARATHYROID; 1.
 KW HORMONE; SIGNAL.
 FT SIGNAL 1 25 BY SIMILARITY.
 FT PROPEP 26 31 BY SIMILARITY.
 FT CHAIN 32 115 PARATHYROID HORMONE.
 SQ SEQUENCE 115 AA; 12957 MW; 16ED0EBC CRC32;
 Query Match 100.0%; Score 28; DB 1; Length 115;
 Best Local Similarity 100.0%;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: Thu Jul 30 10:08:06 1998
 Job time : 7 secs.

MIPS RELEASE

(TM)

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MPSrch_p protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:08:23 1998; MasPar time 3.56 Seconds
59.081 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-6
Description: (1-5) from US08817547A.pep
Perfect Score: 28
Sequence: 1 SVSET 5

Scoring table: PAM 150
Gap 15

Searched: 140542 segs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_protein 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 16.468; Variance 10.714; scale 1.537

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	28	100.0	82	9	030721	1.95e+02
2	28	100.0	110	3	016290	1.95e+02
3	28	100.0	113	9	051810	1.95e+02
4	28	100.0	126	9	P95985	1.95e+02
5	28	100.0	189	3	Q19478	1.95e+02
6	28	100.0	228	2	Q15631	1.95e+02
7	28	100.0	228	10	P97891	1.95e+02
8	28	100.0	228	10	062348	1.95e+02
9	28	100.0	260	3	015744	1.95e+02
10	28	100.0	291	9	028438	1.95e+02
11	28	100.0	338	9	Q44791	1.95e+02
12	28	100.0	350	9	Q47506	1.95e+02
13	28	100.0	377	3	P92126	1.95e+02
14	28	100.0	378	9	031328	1.95e+02
15	28	100.0	389	8	023888	1.95e+02
16	28	100.0	389	8	023882	1.95e+02
17	28	100.0	389	8	Q23883	1.95e+02
18	28	100.0	394	8	Q43809	1.95e+02
19	28	100.0	420	9	Q25039	1.95e+02
20	28	100.0	425	3	Q26973	1.95e+02

RESULT	ID	PRELIMINARY	PRT	82 AA.
1	030721			
2	030721			
3	01-JAN-1998 (TREMBLREL. 05, CREATED)			
4	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
5	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
6	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
7	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
8	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
9	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
10	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
11	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
12	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
13	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
14	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
15	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
16	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
17	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
18	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
19	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
20	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			

ALIGNMENTS

Query Match	Best Local Similarity	Score	DB 9:	Length	82:
Matches	5;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
1	6 SVSET 10				
2	1 SVSET 5				
3	1 SVSET 5				
4	1 SVSET 5				
5	1 SVSET 5				
6	1 SVSET 5				
7	1 SVSET 5				
8	1 SVSET 5				
9	1 SVSET 5				
10	1 SVSET 5				
11	1 SVSET 5				
12	1 SVSET 5				
13	1 SVSET 5				
14	1 SVSET 5				
15	1 SVSET 5				
16	1 SVSET 5				
17	1 SVSET 5				
18	1 SVSET 5				
19	1 SVSET 5				
20	1 SVSET 5				

RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., STILSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
RL NATURE 368:32-38(1994).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL NZ.
RA BECKER M., BRADSHAW H., KRAMER J.,
RL SUBMITTED (Aug-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL NZ.
RA WATERSTON R.,
SUBMITTED (Jul-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
EMBL; AF016427; G2291235; -.
SEQUENCE 110 AA; 13038 MW; 9E338B0B CRC32;

Query Match 100.0%; Score 28; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.95e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 36 SVSEI 40
QY 1 SVSEI 5

Search completed: Thu Jul 30 10:08:48 1998
Job time : 25 secs.

[W][E][R][E]
[T][W]

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:12:14 1998; MasPar time 2.65 Seconds
57.826 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-7
Description: (1-10) from US08817547A.pep
Perfect Score: 73
Sequence: 1 HNLGKHLNSM 10

Scoring table: PAM 150
Gap 15

Searched: 124785 segs, 15338987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 16.178; Variance 63.374; scale 0.355

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	73	100.0	28	4	R23064 Modified hPTH(7-34)-NH	1.59e+00
2	73	100.0	34	14	R74521 Human parathyroid hor	1.59e+00
3	73	100.0	34	22	W17957 Human parathyroid hor	1.59e+00
4	73	100.0	34	22	W17954 Human parathyroid hor	1.59e+00
5	73	100.0	34	22	W17968 Human parathyroid hor	1.59e+00
6	73	100.0	34	22	W17950 Human PTH analogue [C	1.59e+00
7	73	100.0	34	22	W17969 Human parathyroid hor	1.59e+00
8	73	100.0	34	22	W17951 Human parathyroid hor	1.59e+00
9	73	100.0	34	10	R55724 Parathormone N-termin	1.59e+00
10	73	100.0	34	7	R34457 Human parathyroid hor	1.59e+00
11	73	100.0	34	7	R34364 Human parathyroid hor	1.59e+00
12	73	100.0	34	19	R98951 Target peptide (PTH(1	1.59e+00
13	73	100.0	34	7	R34363 Human parathyroid hor	1.59e+00
14	73	100.0	34	22	W17955 Human parathyroid hor	1.59e+00
15	73	100.0	34	22	W17947 Human parathyroid hor	1.59e+00
16	73	100.0	34	22	W20000 Cyclised human parath	1.59e+00
17	73	100.0	36	9	R58290 [Ala26]-hPTH(1-36)-NH	1.59e+00
18	73	100.0	36	9	R58295 [D-Val35]-hPTH(1-36)-	1.59e+00
19	73	100.0	36	9	R58175 [Pyridine-2-carboxyl	1.59e+00

20	73	100.0	36	9	R58253 [4-aminobenzoic acid1	1.59e+00
21	73	100.0	36	9	R58252 [Asn1]-hPTH(1-36)-NH2	1.59e+00
22	73	100.0	36	9	R58263 [D-Ile5]-hPTH(1-36)-NH	1.59e+00
23	73	100.0	36	9	R58268 [Cha8]-hPTH(1-36)-NH2	1.59e+00
24	73	100.0	36	9	R58297 [Pro35]-hPTH(1-36)-NH	1.59e+00
25	73	100.0	36	9	R58270 [D-Leu11]-hPTH(1-36)-	1.59e+00
26	73	100.0	38	9	R58029 [Leu1]-hPTH(1-38)-OH	1.59e+00
27	73	100.0	38	9	R58143 [Gln21]-hPTH(1-38)-OH	1.59e+00
28	73	100.0	38	9	R58152 [Arg22]-hPTH(1-38)-OH	1.59e+00
29	73	100.0	38	9	R58151 [Ser22]-hPTH(1-38)-OH	1.59e+00
30	73	100.0	38	19	R89558 Target peptide (PTH(1	1.59e+00
31	73	100.0	38	9	R58129 [His19]-hPTH(1-38)-OH	1.59e+00
32	73	100.0	38	9	R58132 [Pro19]-hPTH(1-38)-OH	1.59e+00
33	73	100.0	44	26	P30015 Human parathyroid hor	1.59e+00
34	73	100.0	47	25	W21946 Fusion protein comp1	1.59e+00
35	73	100.0	79	6	R30853 hPTH mutain lacking 5	1.59e+00
36	73	100.0	84	27	W25687 Human parathyroid hor	1.59e+00
37	73	100.0	84	4	R21191 Human parathyroid hor	1.59e+00
38	73	100.0	84	4	R21190 Human parathyroid hor	1.59e+00
39	73	100.0	84	4	R21162 Human parathyroid hor	1.59e+00
40	73	100.0	84	4	R21192 Human parathyroid hor	1.59e+00
41	73	100.0	84	4	R21188 Human parathyroid hor	1.59e+00
42	73	100.0	84	4	R21189 Human parathyroid hor	1.59e+00
43	73	100.0	84	25	W29420 Human parathyroid hor	1.59e+00
44	73	100.0	84	4	R23238 Human parathyroid hor	1.59e+00
45	73	100.0	115	13	R75693 Human prepro-PTH	1.59e+00

ALIGNMENTS

RESULT 1
ID R22064 standard; Protein; 28 AA.
AC R22064;
DT 14-JUL-1992 (first entry)
DE Modified hPTH(7-34)-NH2.
KW Parathyroid hormone; analogue; osteoporosis; hyperthyroidism;
KW tumours; hypercalcaemia; renal failure; human.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_site 7
FT /label= OTHER
FT /note= "OTHER - see comments"
FT modified_site 28
FT /label= NH2
FN US5093233-A.
PD 03-MAR-1992.
PF 25-APR-1990: 514394.
PR 25-APR-1990: US-514394.
PA (MERI) MERCK & CO INC.
PI Rosenblatt M, Koubini E, Chorev M, Nutt RF;
DR WPI; 92-096233/12.
PT New parathyroid hormone analogues - useful for treatment and in
PT vitro diagnosis of PTH-dependent tumours, immune disorders,
PT osteoporosis and hyperparathyroidism.
PS Claim 1; Column 10; 6pp; English
CC The peptide is modified at Lys13 (of the parent PTH) in the epsilon
CC amino acid gp. by N,N-diisobutyl or 3-phenylpropionyl. The PTH
CC analogue binds with high affinity to the peptide hormone receptor
CC without activating the 2nd messenger mol. The modification of the
CC lys residue stabilises the bioactive conformation of PTH to enhance
CC the activity. The peptide may be used in vitro bioassays to
CC measure naturally occurring PTH and to diagnose the etiology of or
CC to treat osteoporosis or hypercalcaemia. It may also be used to
CC treat hyperthyroidism and diseases caused by aberrant prodn. of
CC hormone-like substances, such as tumours. It may also be used to
CC treat immune diseases such as inflammation. It is prepd. by solid
CC phase synthesis.
CC See also R22058-75.
SQ Sequence 28 AA:
Query Match 100.0%; Score 73; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.59e+00;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 hnlqkhlms 12
 |||||
 QY 1 HNLGKHLNSM 10

RESULT 2

ID R74521 standard; Peptide; 34 AA.
 AC R74521;
 DT 04-DEC-1995 (first entry)
 DE Human parathyroid hormone (1-34).
 KW Analogue; truncated human parathyroid hormone; PTH; hPTH; substitution;
 KW osteoporosis; hypercalcaemia; hyperparathyroidism;
 KW metabolic bone disease; human; veterinary medicine;
 KW iontophoretic transdermal transport; recombinant E.coli.
 OS Homo sapiens.
 PN W09511988-A.
 PD 04-MAY-1995
 PE 25-OCT-1994; U12205.
 PF 25-OCT-1993; US-142551.
 (AFY-) AFFYMAX TECHNOLOGIES NV.
 Oldenburg KR, Selick HE;
 WPI; 95-178880/23.
 DR New active analogues of parathyroid hormone - with increased
 PT activity, stability in serum etc., esp. for treating
 PT osteoporosis, also related DNA and vectors
 PS Disclosure; Page 1; 109pp; English.
 CC This sequence represents residues 1-34 of human parathyroid hormone
 CC (hPTH). This sequence was used in the production of analogues of the
 CC truncated form of PTH. These analogues have increased activity and
 CC longer serum half life than native PTH due to eg. substitution of Met
 CC residues with leu residues and replacing the carboxy Phe with Tyr. The
 CC carboxy terminal may also be modified by the addition of a homoserine
 CC residue or analogue, or by the addition of residues 35-84 of wild type
 CC PTH (see R74410). These PTH analogues may be used in the treatment of
 CC osteoporosis or hypercalcaemia, hyperparathyroidism or other metabolic
 CC bone diseases in human or veterinary medicine. These peptides may also
 CC have increased iontophoretic transdermal transport. These peptides may also
 CC PTH and can be produced in high yield in recombinant E.coli.
 SQ Sequence 34 AA;

Query Match 100.0%; Score 73; DB 14; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.59e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 hnlqkhlms 18
 |||||
 QY 1 HNLGKHLNSM 10

Search completed: Thu Jul 30 10:12:36 1998
 Job time : 22 secs.

(42)

COMMENT Resolution: not applicable
COMMENT Determination: NMR
KEYWORDS hormone
FEATURE
15-25 #region helix (right hand alpha)
SUMMARY #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 73; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.13e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Db 6 HNLGKHLNSM 15
|||||
QY 1 HNLGKHLNSM 10

Search completed: Thu Jul 30 10:11:56 1998
Job time : 34 secs.

WATERMAN (TM)

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MPsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:10:15 1998; MasPar time 2.14 Seconds
117.135 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-7
Description: (1-10) from US08817547A.pep
Perfect Score: 73
Sequence: 1 HNLGKHLNSM 10

Scoring table:
PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 23.362; Variance 25.262; scale 0.925

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	73	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	1.53e-06
2	69	94.5	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	1.99e-05
3	62	94.5	115	1	PTHY_CANFA PARATHYROID HORMONE PR	1.99e-05
4	62	84.9	115	1	PTHY_PIG PARATHYROID HORMONE PR	1.50e-03
5	59	80.8	115	1	PTHY_RAT PARATHYROID HORMONE PR	8.86e-03
6	48	65.8	171	1	PALA_BACSU PROTEASE SYNTHASE AND	3.78e+00
7	48	65.8	381	1	DHB2_MOUSE ESTRADIOL 17 BETA-DEHY	3.78e+00
8	48	65.8	887	1	MTS4_SCHPO 26S PROTEASOME REGULAT	3.78e+00
9	47	64.4	187	1	ATPD_ODOSI ATP SYNTHASE DELTA CHA	6.28e+00
10	47	64.4	621	1	PLAK_MOUSE JUNCTION PLAKOGLOBIN (6.28e+00
11	47	64.4	738	1	PLAK_XENLA JUNCTION PLAKOGLOBIN (6.28e+00
12	47	64.4	743	1	PLAK_HUMAN JUNCTION PLAKOGLOBIN (6.28e+00
13	46	63.0	152	1	HMG8_SOYBN HMG-Y RELATED PROTEIN	1.03e+01
14	46	63.0	176	1	HMG8_SOYBN HMG-Y RELATED PROTEIN	1.03e+01
15	46	63.0	192	1	SC72_YEAST TRANSLOCATION PROTEIN	1.03e+01
16	46	63.0	417	1	HS47_RAT 47 KD HEAT SHOCK PROTE	1.03e+01
17	46	63.0	417	1	HS47_HUMAN 47 KD HEAT SHOCK PROTE	1.03e+01
18	46	63.0	417	1	HS47_MOUSE 47 KD HEAT SHOCK PROTE	1.03e+01
19	46	63.0	418	1	CBP2_HUMAN COLLAGEN-BINDING PROTE	1.03e+01
20	46	63.0	2068	1	CCG1_DOMIE TRANSCRIPTION INITIATI	1.03e+01
21	45	61.6	208	1	YFJ1_ECOLI HYPOTHEICAL 24.6 KD P	1.69e+01
22	45	61.6	405	1	HS47_CHICK 47 KD HEAT SHOCK PROTE	1.69e+01
23	45	61.6	700	1	PTPE_HUMAN PROTEIN-TYROSINE PHOSP	1.69e+01

RESULT	ID	PTHY_HUMAN	STANDARD	PTHY	115 AA.	ALIGNMENTS
AC	21-JUL-1986	(REL. 01, CREATED)				
DT	13-AUG-1987	(REL. 05, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).					
GN	PTH.					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
NC	EUTHERIA; PRIMATES.					
CC	[1]					
RP	SEQUENCE FROM N.A.					
RP	MEDLINE: 82150870.					
RA	HENDY G.N., KRONENBERG H.M., POTTS J.T., JR., RICH A.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RP	MEDLINE: 83169834.					
RA	VASICER T.J., MCCREYTT B.E., FREEMAN M.W., FENNICK B.J.,					
RA	HENDY G.N., POTTS J.T., JR., RICH A., KRONENBERG H.M.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 80:2127-2131(1983).					
RN	[3]					
RP	SEQUENCE OF 26-37.					
RA	MEDLINE: 74174967.					
RA	JACOBS J.W., KEMPER B., NIML H.D., HABENER J.F., POTTS J.T., JR.;					
RL	NATURE 249:155-157(1974).					
RN	[4]					
RP	SEQUENCE OF 32-68.					
RP	MEDLINE: 74111656.					
RA	NIML H.D., SAUER R.T., JACOBS J.W., KEUTMANN H.T., SEGRE G.V.,					
RA	O'RIORDAN J.L.H., AUBACH G.D., POTTS J.T., JR.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).					
RN	[5]					
RP	SEQUENCE OF 61-83 AND 84-115.					
RP	MEDLINE: 79082855.					
RA	KEUTMANN H.T., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.,					
RA	POTTS J.T., JR.;					
RL	BIOCHEMISTRY 17:5723-5729(1978).					
RN	[6]					
RP	SEQUENCE OF 75-100.					
RA	KEUTMANN H.T., NIML H.D., JACOBS J.W., BARLING P.M., HENDY G.N.,					
RA	O'RIORDAN J.L.H., POTTS J.T., JR.;					
RL	(IN) CALCULUM-REGULATING HORMONES, TALMADGE R.V., OWEN M.,					
RL	PARSONS J.A., EDS., PP. 9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM,					
RL	(1975).					
RN	[7]					

RP REVIEWS.
RX MEDLINE: 75146516.
RA KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
RL BIOCHEMISTRY 14:1842-1847(1975).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE: 75059220.
RA TREGGAR G.W., VAN RIESCHOTEN J., GREEN E., NIALL H.D.,
RA KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T. JR.;
RL HOPPE-SEYLER S.Z. PHYSIOL. CHEM. 355:415-421(1974).
RN [9]
RP SYNTHESIS OF 32-65.
RX MEDLINE: 73227467.
RA ANDREATTA R.H., HARTMANN A., JOEHL A., KAMBER B., MAIER R.,
RA KUNIGER B., RITTEL W., SIEBER P.;
RL HELV. CHIM. ACTA 56:470-473(1973).
RN [10]
RP STRUCTURE BY NMR OF 32-65.
RX MEDLINE: 91299748.
RA KLAUS W., DIECKMANN T., WRAY V., SCHOMBURG D., WINGENDER E., MAYER H.;
RL BIOCHEMISTRY 30:6936-6942(1991).
RN [11]
RP STRUCTURE BY NMR OF 32-65.
RX MEDLINE: 93345518.
RA BARDEN J.A., CUTHBERTSON R.M.;
RL EUR. J. BIOCHEM. 215:315-321(1993).
RN [12]
RP STRUCTURE BY NMR OF 32-68.
RX MEDLINE: 95318084.
RA MARX U.C., AUSTERMANN S., BAYER P., ADERMAN K., EICHAUT A.,
RA STICHT H., WALTER S., SCHMID F.-X., JENICKE R., FORSMANN W.-G.,
RA ROESCH P.;
RL J. BIOL. CHEM. 270:15194-15202(1995).
RN [13]
RP VARIANT ARG-18.
RX MEDLINE: 91009811.
RA ANNOUD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,
RA KRONENBERG H.M.;
RL J. CIN. INVEST. 86:1084-1087(1990).
RN [14]
RP FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
CC HYPOPARATHYROIDISM (FTH).
EMBL: J00301: G190704: -;
DR EMBL: V00597: G37144: -;
DR EMBL: A29146: E186700: -;
DR PIR: A01536: PTHU.
DR PIR: A19339: A19339.
DR PDB: 1HPH: 10-JUL-95.
DR PDB: 1HTH: 15-OCT-97.
DR PDB: 12WA: 12-MAR-97.
DR PDB: 12WB: 12-MAR-97.
DR PDB: 12WC: 12-MAR-97.
DR PDB: 12WD: 12-MAR-97.
DR PDB: 12WE: 12-MAR-97.
DR PDB: 12WF: 16-JUN-97.
DR PDB: 12WG: 16-JUN-97.
DR PDB: 12WG: 16-JUN-97.
DR MTM: 146200: -;
DR MTM: 168450: -;
DR PROSITE: PS00335: PARATHYROID; 1.
DR HORMONE: SIGNAL; DISEASE MUTATION; 3D-STRUCTURE.
FT SIGNAL 1 25
FT PROPER 26 31
FT CHAIN 32 115
FT VARIANT 18 18
FT CONFLICT 107 107
FT SEQUENCE 115 AA: 12861 MM: 243887CT CRC32;
N -> D (IN REF. 5).
N -> D (IN REF. 5).
Query Match 100.0%; Score 73; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 1,53e-06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 40 HNLGKHLNSM 49
QY 1 HNLGKHLNSM 10
RESULT 2
ID PTHV BOVIN STANDARD: PRT: 115 AA.
AC P01268;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 80056617.
RA KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
RA POTTS J.T. JR., RICH A.;
RL PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 82037785.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 83105964.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL MOL. CELL. ENDOCRINOL. 28:411-424(1982).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE: 84262483.
RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
RL GENE 28:319-329(1984).
RN [5]
RP SEQUENCE OF 26-115.
RX MEDLINE: 74142666.
RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,
RA COHN D.V.;
RL PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
RN [6]
RP SEQUENCE OF 32-115.
RX MEDLINE: 71076162.
RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,
RA AURBACH G.D., POTTS J.T. JR.;
RL HOPPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).
RN [7]
RP SEQUENCE OF 32-115.
RX MEDLINE: 71063634.
RA BREWER H.B. JR., ROMAN R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE: 71091588.
RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
RA DEFLOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
EMBL: V00106: G85: -;
DR EMBL: J00023: G163641: -;
DR EMBL: J00024: G163643: -;
DR EMBL: J00024: E18249: ALT_SEQ.
DR EMBL: J00024: E18250: ALT_INIT.
DR EMBL: K01938: G163647: -;
DR EMBL: M25082: G163645: -;
DR PIR: A01536: PTHO.
DR PIR: A24949: A24949.
DR PROSITE: PS00335: PARATHYROID; 1.
DR HORMONE: SIGNAL.

FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT CONFLICT 106 106
 SQ SEQUENCE 115 AA; 12980 MM; 673EA5F2 CRC32;
 PARATHYROID HORMONE.
 V -> G (IN REF. 4).

Query Match 94.5%; Score 69; DB 1; length 115;
 Best Local Similarity 90.0%; Pred. No. 1.99e-05;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 40 HNLGKRLSSM 49
 |||||:|
 QY 1 HNLGKRLNSM 10

Search completed: Thu Jul 30 10:10:23 1998
 Job time : 8 secs.



RL MOL. CELL. BIOL. 6:411-424(1986).
 DR EMBL: M13100; G804811; .
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 367 AA; 43685 MW; 3D4A69E5 CRC32;

Query Match 68.5%; Score 50; DB 10; Length 367;
 Best Local Similarity 66.7%;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 74 KLGKHLHM 82
 :|||||:
 QY 2 NLGKHLNSM 10

Search completed: Thu Jul 30 10:11:05 1998
 Job time : 24 secs.

WIPED (TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:14:54 1998; MasPar time 2.63 Seconds
52.387 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-8
Description: (1-9) from US08817547A.pep
Perfect Score: 64
Sequence: 1 NLGKHLNSM 9

Scoring table: PAM 150
Gap 15

Searched: 124785 segs, 15338987 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-genseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 15.754; Variance 55.237; scale 0.285

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	64	100.0	34 22	W17957	Human parathyroid hor	3.96e+00
2	64	100.0	34 22	W17954	Human parathyroid hor	3.96e+00
3	64	100.0	34 22	W17968	Human parathyroid hor	3.96e+00
4	64	100.0	34 22	W17950	Human PTH analogue [C	3.96e+00
5	64	100.0	34 22	W17969	Human parathyroid hor	3.96e+00
6	64	100.0	34 22	W17951	Human parathyroid hor	3.96e+00
7	64	100.0	34 8	R41557	[Gln25,26,27]-hPTH (1-	3.96e+00
8	64	100.0	34 8	R41550	[D-Ala3]-hPTH (1-34).	3.96e+00
9	64	100.0	34 19	R38951	Target peptide (PTH(1	3.96e+00
10	64	100.0	34 22	W17955	Human parathyroid hor	3.96e+00
11	64	100.0	34 22	W17947	Human parathyroid hor	3.96e+00
12	64	100.0	34 22	W20000	Cyclised human parath	3.96e+00
13	64	100.0	36 9	R58272	[D-Lys13]-hPTH(1-36) -	3.96e+00
14	64	100.0	36 9	R58219	[Met26]-hPTH(1-36)-NH	3.96e+00
15	64	100.0	36 9	R58263	[D-Ile5]-hPTH(1-36)-N	3.96e+00
16	64	100.0	36 9	R58268	[Cha8]-hPTH(1-36)-NH2	3.96e+00
17	64	100.0	36 9	R58243	Propargyl-[Al1]-hPTH(1	3.96e+00
18	64	100.0	36 9	R58229	[Ala30]-hPTH(1-36)-NH	3.96e+00
19	64	100.0	36 9	R58290	[Ala26]-hPTH(1-36)-NH	3.96e+00

20	64	100.0	36 9	R58295	[D-Val35]-hPTH(1-36) -	3.96e+00
21	64	100.0	36 9	R58253	[4-aminobenzoic acid1	3.96e+00
22	64	100.0	36 9	R58252	[Asn1]-hPTH(1-36)-NH2	3.96e+00
23	64	100.0	37 9	R58244	[Ala0]-hPTH(1-36)-NH2	3.96e+00
24	64	100.0	38 9	R58148	[Ala22]-hPTH(1-38)-OH	3.96e+00
25	64	100.0	38 9	R58145	[Gly22]-hPTH(1-38)-OH	3.96e+00
26	64	100.0	38 9	R58125	[Leu19]-hPTH(1-38)-OH	3.96e+00
27	64	100.0	38 9	R58134	[Ile19]-hPTH(1-38)-OH	3.96e+00
28	64	100.0	38 9	R58269	[Leu8]-hPTH(1-38)-NH2	3.96e+00
29	64	100.0	38 9	R58024	[Ala1,Ile2]-hPTH(1-38	3.96e+00
30	64	100.0	38 19	R38958	Target peptide (PTH(1	3.96e+00
31	64	100.0	44 26	P30015	Human parathyroid hor	3.96e+00
32	64	100.0	47 25	W21945	Fusion protein complr	3.96e+00
33	64	100.0	84 27	W25687	Human parathyroid hor	3.96e+00
34	64	100.0	84 4	R21180	Human parathyroid hor	3.96e+00
35	64	100.0	84 4	R21181	Human parathyroid hor	3.96e+00
36	64	100.0	84 4	R21220	Human parathyroid hor	3.96e+00
37	64	100.0	84 4	R21194	Human parathyroid hor	3.96e+00
38	64	100.0	84 8	R42074	Stability-enhanced hu	3.96e+00
39	64	100.0	84 8	R42068	Stability-enhanced hu	3.96e+00
40	64	100.0	84 25	W29420	Human parathyroid hor	3.96e+00
41	64	100.0	84 4	R21175	Human parathyroid hor	3.96e+00
42	64	100.0	84 4	R21174	Human parathyroid hor	3.96e+00
43	64	100.0	84 4	R21231	Human parathyroid hor	3.96e+00
44	64	100.0	84 4	R21202	Human parathyroid hor	3.96e+00
45	64	100.0	84 4	R21158	Human parathyroid hor	3.96e+00

ALIGNMENTS

RESULT 1
ID W17957 standard; peptide; 34 AA.

AC W17957;
DT 29-JUL-1997 (first entry)
DE Human parathyroid hormone analogue [Alb3]-hPTH(1-34)-NH2.
KW Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
KW bone fracture.
OS Homo sapiens.
OS Synthetic.

FT Key Location/Qualifiers
FT modified_site 3
FT modified_site 3 /label= Alb

FT modified_site 34 /note= "In amide form"

PI W09702834-Al.
PD 30-JAN-1997.
PR 03-JUL-1996; U11292.
PR 13-JUL-1995; US-001105.
PR 06-SEP-1995; US-003305.
PR 29-MAR-1996; US-626186.
PA (BIOM-) BIOMEASURE INC.
PI Dong 2X;
DR WPI; 97-11819/11.

PT New variants of human parathyroid hormone 1-34 peptide - which
stimulate bone growth and are used for treatment of osteoporosis and
bone fracture.
PS Claim 11; Page -: 33p; English.
CC The present sequence is a specific example of a human parathyroid
hormone (hPTH) analogue from fragment 1-34 in which at least one
of the amino acid residues at positions 3, 12, 16, 17, 19 and 34
is alpha-aminoisobutyric acid (Aib). In this example the Ser residue
at position 3 of the wild-type has been substituted by Aib. The hPTH
analogues stimulate bone growth and so are useful in human or veterinary
medicine for treatment of osteoporosis and bone fracture, optionally in
conjunction with anti-resorptive therapy (bisphosphonates and
calcitonin).
CC N.B. The present sequence does not appear in the specification. It
corresponds to the known hPTH 1-34 fragment with the modifications
as stated in the claim.
SQ Sequence 34 AA;

Query Match 100.0%; Score 64; DB 22; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.96e+00;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 nlghlnsm 18

QY 1 NLGRHLNSM 9

RESULT 2

ID M17954 standard; peptide; 34 AA.

AC M17954; 29-JUL-1997 (first entry)

DE Human parathyroid hormone analogue [Alb19]hPTH(1-34)NH₂.

KW Osteoporosis; agonist; PTH; human; anti-resorptive therapy;

OS bone fracture.

OS Homo sapiens.

OS Synthetic.

FT Key

FT modified_site

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Search completed: Thu Jul 30 10:15:09 1998
Job time : 15 secs.

WO9702834-A1. /note= "In amide form"
30-JAN-1997.
03-JUL-1996; U11292.
PR 13-JUL-1995; US-001105.
PR 06-SEP-1995; US-003305.
PR 29-MAR-1996; US-626186.
PA (BIO-M-) BIOMEASURE INC.
PI Dong ZX;
DR WPI; 97-11819/11.
PT New variants of human parathyroid hormone 1-34 peptide - which
PT stimulate bone growth and are used for treatment of osteoporosis and
PT bone fracture
PS Claim 11; Page -: 33pp; English.
CC The present sequence is a specific example of a human parathyroid
CC hormone (hPTH) analogue from fragment 1-34 in which at least one
CC of the amino acid residues at positions 3, 12, 16, 17, 19 and 34
CC is alpha-aminoisobutyric acid (Aib). In this example the Glu residue
CC at position 19 of the wild-type has been substituted by Aib. The hPTH
CC analogues stimulate bone growth and so are useful in human or veterinary
CC medicine for treatment of osteoporosis and bone fracture, optionally in
CC conjunction with anti-resorptive therapy (bisphosphonates and
CC calcitonin).
CC N.B. The present sequence does not appear in the specification. It
CC corresponds to the known hPTH 1-34 fragment with the modifications
CC as stated in the claim.
SQ Sequence 34 AA.

Query Match 100.0%; Score 64; DB 22; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.96e+00;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 nlghlnsm 18

QY 1 NLGRHLNSM 9

COMMENT Resolution: not applicable
 COMMENT Determination: NMR
 KEYWORDS hormone
 FEATURE 15-25
 SUMMARY #region helix (right hand alpha) #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 64; DB 5; Length 34;
 Best local similarity 100.0%; Pred. NO. 2.46e-03;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 7 NLGKHLNSM 15
 QY 1 NLGKHLNSM 9

Search completed: Thu Jul 30 10:14:37 1998
 Job time : 19 secs.

WILEY
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:13:18 1998; MasPar time 3.76 Seconds
Tabular output not generated. 100.904 Million cell updates/sec

Title: >US-08-817-547A-8
Description: (1-9) from US08817547A.pap
Perfect Score: 64
Sequence: 1 NLGKHLNSM 9

Scoring table:
Gap 15
PAM 150

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 21.703; Variance 22.712; scale 0.956

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	50	78.1	105	10	063473	PARATHYROID HORMONE (F	5.27e-01
2	50	78.1	367	10	063778	HYPOTHETICAL 43.7 KD P	5.27e-01
3	50	78.1	513	10	063789	L1 RETROPOSON, ORF2 MR	5.27e-01
4	50	78.1	1300	10	P97692	L1 RETROTRANSPOSON ORF	5.27e-01
5	48	75.0	437	6	Q36379	ATP SYNTHASE A CHAIN (1.63e+00
6	47	73.4	421	9	Q28532	HYPOTHETICAL 48.5 KD P	2.84e+00
7	47	73.4	619	1	099234	CHROMOSOME XV READING	2.84e+00
8	46	71.9	472	3	Q09656	HYPOTHETICAL 52.6 KD P	4.91e+00
9	46	71.9	1708	9	Q26769	MAGNESIUM CHELATASE SU	4.91e+00
10	45	70.3	186	9	Q25653	SITE-SPECIFIC RECOMBIN	8.41e+00
11	45	70.3	385	3	018326	HUNCHBACK GAP (FRAGMEN	8.41e+00
12	45	70.3	545	9	Q32006	YOKA PROTEIN.	8.41e+00
13	45	70.3	671	9	Q45597	FUNCTION UNKNOWN.	8.41e+00
14	44	68.8	82	4	Q29248	APOLIPROTEIN A-1 (FR	1.43e+01
15	44	68.8	242	11	Q80897	COMPLETE GENOME (FRAG	1.43e+01
16	44	68.8	301	11	Q70212	ENVELOPE GLYCOPROTEIN,	1.43e+01
17	44	68.8	325	9	Q26290	LACTATE DEHYDROGENASE.	1.43e+01
18	44	68.8	545	11	Q90054	ORF2.	1.43e+01
19	43	67.2	171	2	Q15093	PLAOGLOBIN (FRAGMENT)	2.40e+01
20	43	67.2	443	9	P76507	FROM BASES 2458322 TO	2.40e+01

21	43	67.2	518	12	Q13035	PROSAPOSIN.	2.40e+01
22	43	67.2	534	3	Q23651	ZK853.3.	2.40e+01
23	43	67.2	646	10	063779	HYPOTHETICAL 76.2 KD P	2.40e+01
24	43	67.2	719	3	Q17828	CORF8.2.	2.40e+01
25	43	67.2	745	10	P70565	PLAOGLOBIN.	2.40e+01
26	43	67.2	745	2	Q15151	PLAOGLOBIN.	2.40e+01
27	43	67.2	979	3	Q21962	SIMILAR TO GLYCINE DEH	2.40e+01
28	43	67.2	1854	10	Q65131	RAT LUNG-DERIVED L01 C	2.40e+01
29	43	67.2	2294	2	Q15265	PROTEIN TYROSINE PHOSP	2.40e+01
30	43	67.2	2317	10	Q63130	RAT LUNG-DERIVED C-ROS	2.40e+01
31	43	67.2	2338	10	Q63132	RAT HEART-DERIVED C-RO	2.40e+01
32	43	67.2	2340	10	Q64736	ROSI PROTOONCOGENE (C-RO	2.40e+01
33	43	67.2	2340	10	Q67705	ROSI PROTOONCOGENE (PR	2.40e+01
34	43	67.2	2450	10	Q62135	PROTEIN-TYROSINE PHOSP	2.40e+01
35	43	67.2	2460	10	Q64512	PROTEIN TYROSINE PHOSP	2.40e+01
36	43	67.2	2466	2	Q15264	PROTEIN TYROSINE PHOSP	2.40e+01
37	43	67.2	2466	2	Q16826	PROTEIN-TYROSINE-POSP	2.40e+01
38	43	67.2	2484	4	Q28006	BAL TYROSINE PHOSPHAT	2.40e+01
39	43	67.2	2485	2	Q15263	PROTEIN TYROSINE PHOSP	2.40e+01
40	43	67.2	2490	2	Q15223	PROTEIN TYROSINE PHOSP	2.40e+01
41	42	65.6	290	9	Q03086	REPLICATION PROTEIN A	4.00e+01
42	42	65.6	1071	11	P89047	POLYPROTEIN (FRAGMENT)	4.00e+01
43	42	65.6	2251	3	Q22190	T05A10.1.	4.00e+01
44	42	65.6	2589	11	Q66776	POLYPROTEIN.	4.00e+01
45	42	65.6	3896	11	P87514	PESTIVIRUS POLYPROTEIN	4.00e+01

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	105 AA.
AC	063473:			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE (FRAGMENT).			
GN	PTH.			
OS	RATTUS NORVEGICUS (RAT).			
OC	EUMAROTIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUMAROTIA; RODENTIA.			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RC	TISSUE-TYROID, AND PARATHYROID;			
RA	SCHMELZER H.J., GROSS G., MAYER H.;			
RL	ADV. GENE TECHNOL. 21:228-229(1984).			
DR	EMBL; M54875; G601933; -.			
FT	NON TER			
FT	SEQUENCE 105 AA: 11746 MW: 6AC3163E CRC32;			
Query Match		78.1%	Score 50;	DB 10;
Best Local Similarity		77.8%	Pred. No. 5.27e-01;	
Matches	7;	Conservative	1;	Mismatches 1;
			Indels	0;
			Gaps	0;
DB	31 NLGKHLASV 39			
OY	1 NLGKHLNSM 9			
RESULT	2			
ID	063778:	PRELIMINARY	PRT:	367 AA.
AC	063778:			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)			
DE	HYPOTHETICAL 43.7 KD PROTEIN.			
OS	RATTUS NORVEGICUS (RAT)			
OC	EUMAROTIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUMAROTIA; RODENTIA.			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RC	TISSUE-LIVER;			
RX	MEDLINE: 87064324.			
RA	D'AMEROSIO E., WAITZKIN S.D., WINNEY F.R., SALEMME A., FURANO A.V.;			

RL MOL. CELL. BIOL. 6:411-424(1986).
 DR EMBL: M13100; G80481; -
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 367 AA; 43685 MW; 3D4A69E5 CRC32;

Query Match 78.1%; Score 50; DB 10; Length 367;
 Best Local Similarity 66.7%; Pred. No. 5,27e-01;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 74 KIKKHEHM 82
 QY 1 NLGRHLNSM 9

Search completed: Thu Jul 30 10:14:00 1998
 Job time : 42 secs.

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(TM)

MSprch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:12:53 1998; Maspar time 2.12 Seconds
106.569 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-8
Description: (1-9) from US08817547A.pep
Perfect Score: 64
Sequence: 1 NLGKHLNSM 9

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 22.743; Variance 23.428; scale 0.971

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	64	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	1.05e-04
2	60	93.8	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	1.35e-03
3	60	93.8	115	1	PTHY_CANFA PARATHYROID HORMONE PR	1.35e-03
4	53	82.8	115	1	PTHY_PIG PARATHYROID HORMONE PR	9.45e-02
5	50	78.1	115	1	PTHY_PAT PARATHYROID HORMONE PR	5.29e-01
6	46	71.9	152	1	HMG-SOYBN HMG-Y RELATED PROTEIN	4.71e+00
7	46	71.9	176	1	HMG-SOYBN HMG-Y RELATED PROTEIN	4.71e+00
8	46	71.9	192	1	SC72 YEAST TRANSCRIPTION INITIAT	4.71e+00
9	46	71.9	2068	1	CGGL DROME TRANSCRIPTION INITIAT	4.71e+00
10	45	70.3	208	1	YFJL ECOLI HYPOHETICAL 24.6 KD P	7.96e+00
11	45	70.3	700	1	PTPE_HUMAN PROTEIN-TYROSINE PHOSP	7.96e+00
12	45	70.3	985	1	NAH_YEAST PROBABLE NA(+)/H(+) AN	7.96e+00
13	44	68.8	265	1	APAL_PIG APOLIPROTEIN A-1 PRE	1.33e+01
14	44	68.8	298	1	YHBY ECOLI HYPOHETICAL 33.2 KD P	1.33e+01
15	44	68.8	585	1	Y187 MYCGE HYPOHETICAL ABC TRANS	1.33e+01
16	44	68.8	936	1	YKZK YEAST HYPOHETICAL 106.5 KD	1.33e+01
17	44	68.8	2105	1	POLR_ASCVP GENOME POLYPROTEIN (CN	1.33e+01
18	43	67.2	139	1	STBH_PESM PLASID STABILITY PROT	2.21e+01
19	43	67.2	187	1	ATPD_OOSI ATP SYNTHASE DELTA CHA	2.21e+01
20	43	67.2	313	1	LDH_MERJA L-LACTATE DEHYDROGENAS	2.21e+01
21	43	67.2	462	1	CISY_TETTH CITRATE SYNTHASE, MITO	2.21e+01
22	43	67.2	621	1	PLAK_MOUSE JUNCTION PLAKGLOBIN (2.21e+01
23	43	67.2	738	1	PLAK_XENLA JUNCTION PLAKGLOBIN (2.21e+01

RESULT	ID	PTHY_HUMAN	STANDARD:	PRT:	115 AA.	ALIGNMENTS
AC	24	21-JUL-1986 (REL. 01, CREATED)				
DT	25	13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)				
DT	26	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	27	PARATHYROID HORMONE PRECURSOR (PARATHYRLIN) (PTH).				
GN	28	PTH.				
OS	29	HOMO SAPIENS (HUMAN).				
OC	30	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
CC	31	EUPHERIA; PRIMATES.				
RN	32	SEQUENCE FROM N.A.				
RX	33	MEDLINE: 82150870.				
RA	34	HENDY G.N., KRONENBERG H.M., POTTS J.T. JR., RICH A.;				
RL	35	PROC. NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).				
RN	36	SEQUENCE FROM N.A.				
RX	37	MEDLINE: 83169834.				
RA	38	VASICER T.J., MCCEVITT B.E., FREEMAN M.W., FENNICK B.J.;				
RL	39	HENDY G.N., POTTS J.T. JR., RICH A., KRONENBERG H.M.;				
RL	40	PROC. NATL. ACAD. SCI. U.S.A. 80:2127-2131(1983).				
RN	41	SEQUENCE OF 26-37.				
RX	42	MEDLINE: 74174967.				
RA	43	JACOBS J.W., KEMPER B., NIAL H.D., HABENER J.F., POTTS J.T. JR.;				
RL	44	NATURE 249:155-157(1974).				
RN	45	SEQUENCE OF 32-68.				
RX	46	MEDLINE: 74111656.				
RA	47	NIAL H.D., SAUER R.T., JACOBS J.W., KEUTMANN H.T., SEGRE G.V.;				
RL	48	O'RIORDAN J.L.H., AUBACH G.D., POTTS J.T. JR.;				
RL	49	PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).				
RN	50	SEQUENCE OF 61-83 AND 84-115.				
RX	51	MEDLINE: 79082855.				
RA	52	KEUTMANN H.T., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.;				
RL	53	POTTS J.T. JR.;				
RL	54	BIOCHEMISTRY 17:5723-5729(1978).				
RN	55	SEQUENCE OF 75-100.				
RA	56	KEUTMANN H.T., NIAL H.D., JACOBS J.W., BARLING P.M., HENDY G.N.;				
RL	57	O'RIORDAN J.L.H., POTTS J.T. JR.;				
RL	58	(IN) CALCULUM-REGULATING HORMONES, TALMADGE R.V., OWEN M.;				
RL	59	PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM,				
RL	60	(1975).				
RL	61	[7]				

FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT CONFLICT 106 106
 SQ SEQUENCE 115 AA; 12980 MW; 673EA5F2 CRC32;

Query Match 93.8%; Score 60; DB 1; Length 115;
 Best Local Similarity 88.9%; Pred. No. 1.35e-03;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 41 NLGKHLSSM 49
 QY 1 NLGKHLNSM 9

Search completed: Thu Jul 30 10:12:59 1998
 Job time : 6 secs.



M1050E10
(TW)

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Mpsrch_pp protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:17:12 1998; MasPar time 2.69 Seconds
45.680 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-9
Description: (1-8) from US08817547A.pep
Perfect Score: 59
Sequence: 1 LGKHLNSM 8

Scoring table: PAM 150
Gap 15

Searched: 124785 segs, 15338987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 15.458; Variance 50.932; scale 0.303
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	59	100.0	34 22	W20000	Cyclised human parath	7.14e+00
2	59	100.0	34 22	W17949	Human parathyroid hor	7.14e+00
3	59	100.0	34 22	W17955	Human parathyroid hor	7.14e+00
4	59	100.0	34 22	W17950	Human parathyroid hor	7.14e+00
5	59	100.0	34 7	R34355	Human parathyroid hor	7.14e+00
6	59	100.0	34 22	W17959	Human parathyroid hor	7.14e+00
7	59	100.0	34 22	W17951	Human parathyroid hor	7.14e+00
8	59	100.0	34 4	R22293	Human parathyroid hor	7.14e+00
9	59	100.0	34 8	R41557	[Gln25,26,27]hPTH (1-	7.14e+00
10	59	100.0	34 8	R41550	[D-Ala3]hPTH (1-34).	7.14e+00
11	59	100.0	34 19	R89951	Target peptide (PTH(1	7.14e+00
12	59	100.0	34 22	W17948	Human parathyroid hor	7.14e+00
13	59	100.0	34 22	W17947	Human parathyroid hor	7.14e+00
14	59	100.0	34 22	W17957	Human parathyroid hor	7.14e+00
15	59	100.0	36 9	R58263	[D-Ile5]-hPTH(1-36)-N	7.14e+00
16	59	100.0	36 9	R58268	[Cha8]-hPTH(1-36)-NH2	7.14e+00
17	59	100.0	36 9	R58229	[Ala30]-hPTH(1-36)-NH	7.14e+00
18	59	100.0	36 9	R58297	[Pro35]-hPTH(1-36)-NH	7.14e+00
19	59	100.0	36 9	R58295	[D-Val35]-hPTH(1-36)-	7.14e+00

20	59	100.0	36 9	R58233	[D-His32]-hPTH(1-36)-	7.14e+00
21	59	100.0	36 9	R58252	[Asn1]-hPTH(1-36)-NH2	7.14e+00
22	59	100.0	37 9	R58244	[Ala0]-hPTH(1-36)-NH2	7.14e+00
23	59	100.0	38 9	R58148	[Ala22]-hPTH(1-38)-OH	7.14e+00
24	59	100.0	38 9	R58145	[Gly22]-hPTH(1-38)-OH	7.14e+00
25	59	100.0	38 5	P20248	Parathyroid hormone 1	7.14e+00
26	59	100.0	38 9	R58134	[Ile19]-hPTH(1-38)-OH	7.14e+00
27	59	100.0	38 9	R58075	[Ser33]-hPTH(1-38)-OH	7.14e+00
28	59	100.0	38 19	R89958	Target peptide (PTH(1-	7.14e+00
29	59	100.0	38 9	R58167	[Ile31]-hPTH(1-38)-NH	7.14e+00
30	59	100.0	44 26	P30015	Human parathyroid hor	7.14e+00
31	59	100.0	47 25	W21946	Fusion protein comp1	7.14e+00
32	59	100.0	84 27	W25687	Human parathyroid hor	7.14e+00
33	59	100.0	84 4	R21180	Human parathyroid hor	7.14e+00
34	59	100.0	84 4	R21181	Human parathyroid hor	7.14e+00
35	59	100.0	84 4	R21220	Human parathyroid hor	7.14e+00
36	59	100.0	84 4	R21194	Human parathyroid hor	7.14e+00
37	59	100.0	84 7	R34460	Human parathyroid hor	7.14e+00
38	59	100.0	84 8	R42068	Stability-enhanced hu	7.14e+00
39	59	100.0	84 8	R42074	Stability-enhanced hu	7.14e+00
40	59	100.0	84 25	W29420	Human parathyroid hor	7.14e+00
41	59	100.0	84 4	R21222	Human parathyroid hor	7.14e+00
42	59	100.0	84 4	R21223	Human parathyroid hor	7.14e+00
43	59	100.0	84 4	R23238	Human parathyroid hor	7.14e+00
44	59	100.0	84 4	R21231	Human parathyroid hor	7.14e+00
45	59	100.0	84 4	R21202	Human parathyroid hor	7.14e+00

ALIGNMENTS

RESULT 1
ID W20000 standard; peptide; 34 AA.
AC W20000;
DT 28-AUG-1997 (first entry)
DE Cyclised human parathyroid hormone (1-34) amide.
KW Parathyroid hormone; PTH; amino terminus; cyclic; analogue;
KW adenylate cyclase activity; bone growth; osteoporosis; fracture;
KW antiresorptive therapy.
OS Homo sapiens.
FH Key Location/Qualifiers
FT misc_difference 26 /note= "joined via amide bond to residue 30"
FT misc_difference 30 /note= "joined via amide bond to residue 26"
FT misc_difference 34 /note= "amidated"
FT W09640193-A1.
PD 19-DEC-1996.
PF 06-JUN-1996; U09674.
PR 07-JUN-1995; US-488105.
PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.
PI Chorev M, Rosenblatt M;
DR WPI; 97-051884/05.
PT New cyclic analogues of parathyroid hormone - having di-sulphide or
amide bond between residues 13 and 17 and/or between residues 26 and
30, useful for treating osteoporosis and bone fractures
PS Claim 6; Page -: 23pp; English.
CC W20000 is a cyclised peptide derived from the N-terminal sequence
of human parathyroid hormone (PTH). The peptide is able to bind to
PTH receptors and stimulate adenylate cyclase activity. Cyclised
PTH peptides stimulate bone growth and thus are useful in the
treatment of osteoporosis and bone fractures. Optionally they may
be administered concurrently with antiresorptive therapy (e.g.
CC bisphosphonate and calcitonin).
CC N.B. sequence not given in the specification, created from known
CC sequence of amino acids 1-34 of human PTH.
SQ Sequence 34 AA:
Query Match 100.0%; Score 59; DB 22; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.14e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 11 lgkhlmsm 18

FT	SIGNAL	1	25	
FT	PROPEP	26	31	
FT	CHAIN	32	115	PARATHYROID HORMONE.
FT	CONFLICT	106	106	V -> G (IN REF. 4).
SO	SEQUENCE	115 AA;	12980 MW;	673EAS5F2 CRC32;

Query Match 92.2%; Score 47; DB 1; Length 115;
 Best Local Similarity 83.7%; Pred. No. 1.19e-01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 43 GKHLSSM 49
 ||||:|
 QY 1 GKHLNSM 7

Search completed: Thu Jul 30 10:17:55 1998
 Job time : 8 secs.



WIDEVIEW (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:15:51 1998; MasPar time 3.14 Seconds
93.097 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-9
Description: (1-8) from US08817547A.pep
Perfect Score: 59
Sequence: 1 LGKHLNSM 8

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr56
1:plr1 2:plr2 3:plr3 4:plr4 5:mr13d

Statistics: Mean 21.301; Variance 26.286; scale 0.810

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	59	100.0	34	5 12WA	parathyroid hormone (1.45e-02	
2	59	100.0	34	5 12WE	parathyroid hormone (1.45e-02	
3	59	100.0	34	5 12WG	parathyroid hormone (1.45e-02	
4	59	100.0	34	5 12WF	parathyroid hormone (1.45e-02	
5	59	100.0	35	5 12WD	parathyroid hormone (1.45e-02	
6	59	100.0	36	5 12WB	parathyroid hormone (1.45e-02	
7	59	100.0	37	5 12WH	parathyroid hormone (1.45e-02	
8	59	100.0	37	5 12WC	parathyroid hormone (1.45e-02	
9	59	93.2	115	5 12WC	parathyroid hormone (1.23e-01	
10	55	93.2	115	5 JCA4202	parathyroid hormone (1.23e-01	
11	55	93.2	115	1 PRBO	parathyroid hormone (1.23e-01	
12	49	83.1	513	2 S21976	probable RNA-directed	
13	48	81.4	115	1 PTPE	probable RNA-directed	
14	47	79.7	437	2 S52014	atp6 protein - common	
15	47	79.7	437	2 S48853	H+-transferring ATP s	
16	46	78.0	152	2 S22311	HMG-Y-related protein	
17	46	78.0	176	2 S22310	HMG-Y-related protein	
18	46	78.0	193	2 A53835	SEC63 protein complex	
19	45	76.3	105	2 I51851	parathyroid hormone -	
20	45	76.3	115	2 A05091	parathyroid hormone p	
21	45	76.3	545	2 E69907	DNA recombinase homol	
22	45	76.3	985	2 S53330	Na+/H+-exchanging pro	
23	45	76.3	1490	2 S32373	DNA-binding protein T	

24	45	76.3	2068	2	A47371	transcription initiat	1.75e+01
25	44	74.6	208	2	D65041 <td>hypothetical protein</td> <td>2.78e+01</td>	hypothetical protein	2.78e+01
26	44	74.6	231	2	UQ0704 <td>apolipoprotein A-I -</td> <td>2.78e+01</td>	apolipoprotein A-I -	2.78e+01
27	44	74.6	264	2	S31394 <td>apolipoprotein A-I -</td> <td>2.78e+01</td>	apolipoprotein A-I -	2.78e+01
28	44	74.6	265	2	A46018 <td>apolipoprotein A-I -</td> <td>2.78e+01</td>	apolipoprotein A-I -	2.78e+01
29	44	74.6	325	2	E69118 <td>lactate dehydrogenase</td> <td>2.78e+01</td>	lactate dehydrogenase	2.78e+01
30	44	74.6	619	2	S54636 <td>probable membrane pro</td> <td>2.78e+01</td>	probable membrane pro	2.78e+01
31	44	74.6	671	2	C69621 <td>fructose-bisphosphata</td> <td>2.78e+01</td>	fructose-bisphosphata	2.78e+01
32	44	74.6	700	2	S12053 <td>protein-tyrosine-phos</td> <td>2.78e+01</td>	protein-tyrosine-phos	2.78e+01
33	44	74.6	936	2	S64384 <td>probable membrane pro</td> <td>2.78e+01</td>	probable membrane pro	2.78e+01
34	44	74.6	2105	1	A44059 <td>RNA-directed RNA poly</td> <td>2.78e+01</td>	RNA-directed RNA poly	2.78e+01
35	43	72.9	313	2	B64361 <td>L-lactate dehydrogena</td> <td>4.38e+01</td>	L-lactate dehydrogena	4.38e+01
36	43	72.9	621	2	S35092 <td>plakoglobin - mouse (</td> <td>4.38e+01</td>	plakoglobin - mouse (4.38e+01
37	43	72.9	738	2	S35093 <td>plakoglobin - African</td> <td>4.38e+01</td>	plakoglobin - African	4.38e+01
38	43	72.9	744	2	A32905 <td>plakoglobin, desmosom</td> <td>4.38e+01</td>	plakoglobin, desmosom	4.38e+01
39	43	72.9	1708	2	F69189 <td>magnesium chelatase s</td> <td>6.84e+01</td>	magnesium chelatase s	6.84e+01
40	42	71.2	108	1	RHHUS	somatoliberin precurs	6.84e+01
41	42	71.2	138	2	S66004 <td>transcriptional regul</td> <td>6.84e+01</td>	transcriptional regul	6.84e+01
42	42	71.2	187	2	S25395 <td>H+-transferring ATP s</td> <td>6.84e+01</td>	H+-transferring ATP s	6.84e+01
43	42	71.2	247	2	S72904 <td>phosphoglycerate muta</td> <td>6.84e+01</td>	phosphoglycerate muta	6.84e+01
44	42	71.2	363	2	H69393 <td>iron-sulfur cluster b</td> <td>6.84e+01</td>	iron-sulfur cluster b	6.84e+01
45	42	71.2	762	2	E64597 <td>DNA mismatch repair p</td> <td>6.84e+01</td>	DNA mismatch repair p	6.84e+01

ALIGNMENTS

RESULT 1
ENTRY 12WA #type complete
TITLE parathyroid hormone (residues 1-34) - human
ALTERNATE_NAMES HPTH(1-34)
PDB_TITLE structure of human parathyroid hormone fragment 1-34, NMR 10
STRUCTURES

ORGANISM #formal_name Homo sapiens #common_name man
REFERENCE A67856
#authors Roesch, P.; Marx, U.C.
#submission submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references PDB:12WA
REFERENCE TN00177
#authors Marx, U.C.
#book In Strukturen Verschiedener Parathormonfragmente in Loesung,
pp.0, Bayreuth: University of Bayreuth (Thesis), 1996

COMMENT Resolution: not applicable
KEYWORDS hormone
FEATURE

SUMMARY 6-9 #region helix (right hand alpha)\n19-30 #region helix (right hand alpha)\n#length 34 #molecular-weight 4118 #checksum 5629

Query Match 100.0%; Score 59; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.45e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 11 LGKHLNSM 18
QY 1 LGKHLNSM 8

RESULT 2
ENTRY 12WE #type complete
TITLE parathyroid hormone (residues 4-37) - human
ALTERNATE_NAMES HPTH(4-37)
PDB_TITLE structure of human parathyroid hormone fragment 4-37, NMR 10
STRUCTURES

ORGANISM #formal_name Homo sapiens #common_name man
REFERENCE A67860
#authors Roesch, P.; Marx, U.C.
#submission submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references PDB:12WE
REFERENCE TN001721
#authors Marx, U.C.
#book In Strukturen Verschiedener Parathormonfragmente in Loesung,
pp.0, Bayreuth: University of Bayreuth (Thesis), 1996

COMMENT Resolution: not applicable
 COMMENT Determination: NMR
 KEYWORDS hormone
 FEATURE
 15-25
 SUMMARY

#region helix (right hand alpha)
 #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 59; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.45e-02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 8 LGRHLNSM 15
 QY 1 LGRHLNSM 8

Search completed: Thu Jul 30 10:16:15 1998
 Job time : 24 secs.

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 Msearch - protein database search, using Smith-Waterman algorithm
 on: Thu Jul 30 10:15:27 1998; Maspar time 2.12 Seconds
 Tabular output not generated. 94.808 Million cell updates/sec

Title: >US-08-817-547A-9
 Description: (1-8) from US08817547A.pep
 Perfect Score: 59
 Sequence: 1 LGKHLNSM 8
 Scoring table: PAM 150
 Gap 15
 Searched: 69111 seqs, 25083644 residues
 Post-processing: Minimum Match 0%
 Listing first 45 summaries
 Database: swiss-prot35
 1:swiss1

Statistics: Mean 22.280; Variance 22.155; scale 1.006
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Rank	Score	Match	Length	ID	Description	Pred. No.
1	59	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	9.29e+04
2	55	93.2	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	1.20e+02
3	55	93.2	115	1	PTHY_CANFA PARATHYROID HORMONE PR	1.20e+02
4	48	81.4	115	1	PTHY_PIG PARATHYROID HORMONE PR	8.11e+01
5	46	78.0	152	1	HMGH_SOYBN HMG-Y RELATED PROTEIN	2.51e+00
6	46	78.0	176	1	HMGH_SOYBN HMG-Y RELATED PROTEIN	2.51e+00
7	46	78.0	192	1	SC72_YEAST TRANSLLOCATION PROTEIN	2.51e+00
8	45	76.3	115	1	PTHY_RAT PARATHYROID HORMONE PR	4.37e+00
9	45	76.3	985	1	NAH_YEAST PROBABLE NA(+)/H(+) AN	4.37e+00
10	45	76.3	2068	1	CCGL_DROME TRANSCRIPTION INITIAT	7.51e+00
11	44	74.6	208	1	YETI_BROME HYPOTHETICAL 24.6 KD P	4.37e+00
12	44	74.6	265	1	APRL_PIG APOLIPOPROTEIN A-1 PRE	7.51e+00
13	44	74.6	700	1	PTEP_HUMAN PROTEIN-TYROSINE PHOS	7.51e+00
14	44	74.6	936	1	YGAZ_YEAST HYPOTHETICAL 106.5 KD	7.51e+00
15	44	74.6	2105	1	POLR_YEAST GENOME POLYPROTEIN (CN	7.51e+00
16	43	72.9	313	1	LDH_METJA L-LACTATE DEHYDROGENAS	1.28e+01
17	43	72.9	621	1	PLAK_MOUSE JUNCTION PLAKGLOBIN (1.28e+01
18	43	72.9	738	1	PLAK_XENLA JUNCTION PLAKGLOBIN (1.28e+01
19	43	72.9	743	1	PLAK_HUMAN JUNCTION PLAKGLOBIN (1.28e+01
20	42	71.2	108	1	SLIB_HUMAN SOMATOLIBERIN PRECURSO	2.16e+01
21	42	71.2	138	1	YVAN_BACSV HYPOTHETICAL TRANSCRIP	2.16e+01
22	42	71.2	187	1	ATPD_ODOSI ATP SYNTHASE DELTA CHA	2.16e+01
23	42	71.2	247	1	PMGY_MYCLE PHOSPHOGLYCERATE MUTAS	2.16e+01

ID	Result	1	Standard	PRT	115 AA
AC	POL270;				
DT	21-JUL-1986 (REL. 01, CREATED)				
DT	13-ANG-1987 (REL. 05, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).				
GN	HOMO SAPIENS (HUMAN).				
OS	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; PRIMATES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 82150870.				
RA	HENDY G.N., KRONENBERG H.M., POTTS J.T. JR., RICH A.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 83169834.				
RA	VASICER T.J., MCCREYTT B.E., FREEMAN M.W., FENNICK B.J.;				
RL	HENDY G.N., POTTS J.T. JR., RICH A., KRONENBERG H.M.;				
RN	[3]				
RP	SEQUENCE OF 26-37.				
RX	MEDLINE: 74174967.				
RA	JACOBS J.W., KEMPER B., NIALI H.D., HABENER J.F., POTTS J.T. JR.;				
RL	NATURE 249:155-157(1974).				
RN	[4]				
RP	SEQUENCE OF 32-68.				
RX	MEDLINE: 74111656.				
RA	NIALI H.D., SAUER R.T., JACOBS J.W., KEUTMANN H.T., SEGRE G.V.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).				
RN	[5]				
RP	SEQUENCE OF 61-83 AND 84-115.				
RX	MEDLINE: 79082855.				
RA	KEUTMANN H.T., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.;				
RL	POTTS J.T. JR.;				
RN	[6]				
RP	SEQUENCE OF 75-100.				
RX	KEUTMANN H.T., NIALI H.D., JACOBS J.W., BARLING P.M., HENDY G.				
RA	O'RIORDAN J.L.H., POTTS J.T. JR.;				
RL	(1N) CALCITRIOL-REGULATING HORMONES, TALMADGE R.V., OWEN M.;				
RN	PARSONS J.A., EDS., PP-9-14, EXCERPTA MEDICA FOUNDATION, AMSTERD.				
RL	(1975).				
RN	[7]				

RP REVISIONS.
RX MEDLINE: 75146516.
RA KEUTMANN H.T., NIALI H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
RL BIOCHEMISTRY 14:1842-1847(1975).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE: 75059220.
RA TREGAR G.W., VAN RIJSCHOTEN J., GREEN E., NIALI H.D.,
RA KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T. JR.;
RL HOPPE-SEYLER S. Z. PHYSIOL. CHEM. 355:415-421(1974).
RN [9]
RX SYNTHESIS OF 32-65.
RX MEDLINE: 73227467.
RA ANDRETTA R.H., HARTMAN A., JOEHL A., KAMBER B., MAIER R.,
RA RINKER B., RITTEL W., STEBER P.;
RL HELV. CHIM. ACTA 56:470-473(1973).
RN [10]
RP STRUCTURE BY NMR OF 32-65.
RX MEDLINE: 91299748.
KLAUS W., DIECKMANN T., WRAY V., SCHOMBURG D., WINGENDER E., MAYER H.;
BIOCHEMISTRY 30:6936-6942(1991).
RN [11]
RP STRUCTURE BY NMR OF 32-65.
RX MEDLINE: 93345518.
RA BARDEN J.A., CUTHBERTSON R.M.;
RL EUR. J. BIOCHEM. 215:315-321(1993).
RN [12]
RP STRUCTURE BY NMR OF 32-68.
RX MEDLINE: 95318084.
RA MARX U.C., AUSTERMANN S., BAYER P., ADESMANN K., ECHART A.,
RA STICHT H., WALTER S., SCHMID F.X., JAENITKE R., FORSMANN W.-G.,
RA ROESCH P.;
RL J. BIOL. CHEM. 270:15194-15202(1995).
RN [13]
RP VARIANT ARG-18.
RX MEDLINE: 91009811.
RA ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,
RA KRONENBERG H.M.;
RL J. CLIN. INVEST. 86:1084-1087(1990).
RN [14]
RP FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
CC HYPOPARATHYROIDISM (FTH).
CC EMBL: 300301; G190704; -;
DR EMBL: V00597; G37144; -;
DR EMBL: A29146; E186700; -;
DR PIR: A01536; PTHU.
DR PIR: A19339; A19339.
DR PDB: 1HPH: 10-JUL-85.
DR PDB: 1HTI: 15-OCT-97.
DR PDB: 1ZWA: 12-MAR-97.
DR PDB: 1ZWB: 12-MAR-97.
DR PDB: 1ZWC: 12-MAR-97.
DR PDB: 1ZWD: 12-MAR-97.
DR PDB: 1ZWE: 12-MAR-97.
DR PDB: 1ZWF: 16-JUN-97.
DR PDB: 1ZWG: 16-JUN-97.
DR MTM: 146200; -;
DR MTM: 168450; -;
DR PROSITE: PS00335; PARATHYROID: 1.
KW HORMONE: SIGNAL; DISEASE MUTATION: 3D-STRUCTURE.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115
FT VARIANT 18 18
FT CONFLICT 107 107
SQ SEQUENCE 115 AA; 12861 MW; 243E8/C7 CRC32;
Query Match 100.0%; Score 59; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 9,298-04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 42 LGKHLNSM 49
QY 1 LGKHLNSM 8
RESULT 2
ID PTYX_BOVIN STANDARD; PRT; 115 AA.
AC P01266;
DE 21-JUL-1986 (REL. 01, CREATED)
DE 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE PRECURSOR (PARATHIRIN) (PTH).
CN PTH.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 80056617.
RA KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
RA POTTS J.T. JR., RICH A.;
RL PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 82037785.
RA WEAYER C.A., GORDON D.F., KEMPER B.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 83105964.
RA WEAYER C.A., GORDON D.F., KEMPER B.;
RL MOL. CELL. ENDOCRINOL. 28:411-424(1982).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE: 84262483.
RA WEAYER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
RL GENE 28:319-329(1984).
RN [5]
RP SEQUENCE OF 26-115.
RX MEDLINE: 74142666.
RA HAMILTON J.W., NIALI H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,
RA COHN D.V.;
RL PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
RN [6]
RP SEQUENCE OF 32-115.
RX MEDLINE: 71076162.
RA NIALI H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAMSON B.F.,
RA AURBACH G.D., POTTS J.T. JR.;
RL HOPPE-SEYLER S. Z. PHYSIOL. CHEM. 351:1586-1588(1970).
RN [7]
RP SEQUENCE OF 32-115.
RX MEDLINE: 71063634.
RA BREWER H.B. JR., ROMAN R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE: 71091588.
RA POTTS J.T. JR., TREGAR G.W., KEUTMANN H.T., NIALI H.D., SAUER R.,
RA DEFOS L.J., DAMSON B.F., HOGAN M.L., AURBACH G.D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
RN [9]
RP FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC EMBL: J00106; G85; -;
DR EMBL: J00023; G163641; -;
DR EMBL: J00024; G163643; -;
DR EMBL: J00024; E18249; ALT_SEQ.
DR EMBL: J00024; E18250; ALT_INIT.
DR EMBL: K01398; G163647; -;
DR EMBL: M25082; G163645; -;
DR PIR: A01534; PTHO.
DR PIR: A24949; A24949.
DR PROSITE: PS00335; PARATHYROID: 1.
KW HORMONE: SIGNAL.

FT SIGNAL 1 25
 FT PROPER 26 31
 FT CHAIN 32 115
 FT CONFLICT 106 106
 SQ SEQUENCE 115 AA; 12980 MM; 673EA5F2 CRC32;
 PARATHYROID HORMONE.
 V -> G (IN REF. 4).

Query Match 93.2%; Score 55; DB 1; length 115;
 Best Local Similarity 87.5%; Pred. No. 1.20e-02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 42 LGKHLISM 49
 |||||:
 OY 1 LGKHLISM 8

Search completed: Thu Jul 30 10:15:34 1998
 Job time : 7 secs.

WIPESORT
(TM)

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Mpsrch_Dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:16:32 1998; Maspar time 3.68 Seconds
Tabular output not generated. 91.451 Million cell updates/sec

Title: >US-08-817-547A-9
Description: (1-8) from US08817547A.pep
Perfect Score: 59
Sequence: 1 LGKHLNSM 8

Scoring table: PAM 150
Gap 15

Searched: 140542 segs. 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 21.247; Variance 21.504; scale 0.988

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	49	83.1	367	10	063778	HYPOTHETICAL 43.7 KD P	4.51e-01
2	49	83.1	513	10	063289	L1 RETROPOSON, ORF2 NR	4.51e-01
3	49	83.1	1300	10	P97692	L1 RETROTRANSPOSON ORF	4.51e-01
4	47	79.7	437	6	036379	ATP SYNTHASE A CHAIN (1.45e+00
5	46	78.0	472	3	009656	HYPOTHETICAL 52.6 KD P	2.58e+00
6	45	76.3	105	10	063473	PARATHYROID HORMONE (F	4.53e+00
7	45	76.3	545	9	032006	YOKA PROTEIN	4.53e+00
8	44	74.6	82	4	028248	APOLIPOPROTEIN A-1 (FR	7.90e+00
9	44	74.6	242	11	080897	COMPLETE GENOME (FRAG	7.90e+00
10	44	74.6	301	11	070212	ENVELOPE GLYCOPROTEIN	7.90e+00
11	44	74.6	325	9	026290	LACTATE DEHYDROGENASE	7.90e+00
12	44	74.6	619	1	099234	CHROMOSOME XV READING	7.90e+00
13	44	74.6	671	9	045597	FUNCTION UNKNOWN	7.90e+00
14	43	72.9	171	2	015093	PLAKOGLOBIN (FRAGMENT)	1.36e+01
15	43	72.9	554	3	023651	ZK863.3	1.36e+01
16	43	72.9	719	3	017828	C08F8.2	1.36e+01
17	43	72.9	745	3	015151	PLAKOGLOBIN	1.36e+01
18	43	72.9	745	10	P70565	PLAKOGLOBIN	1.36e+01
19	43	72.9	1708	9	026769	MAGNESIUM CHELATASE SU	1.36e+01
20	42	71.2	107	10	060549	GROWTH HORMONE-RELEASE	2.33e+01

RESULT	ID	SP	PRELIMINARY	PRT	367 AA	ALIGNMENTS
AC	063778					
DT	01-NOV-1996	(TREMBLREL. 01, CREATED)				
DT	01-NOV-1996	(TREMBLREL. 01, LAST SEQUENCE UPDATE)				
DT	01-NOV-1996	(TREMBLREL. 01, LAST SEQUENCE UPDATE)				
DE	HYPOTHETICAL 43.7 KD PROTEIN					
OS	RATTUS NORVEGICUS (RAT)					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE-LIVER:					
RX	MEDLINE: 87064324.					
RA	D'AMBROSIO E., WAITZKIN S.D., WITNEY F.R., SALEME A., FURANO A.V.;					
RL	MOL. CELL. BIOL. 6:411-424(1986).					
DR	EMBL: M13100; G804811; -					
KW	HYPOTHETICAL PROTEIN.					
SO	SEQUENCE 367 AA; 43685 MW; 3D4A69E5 CRC32;					

Query Match	Score	DB	Length	367;
Best Local Similarity	75.0%;	Pred. No. 4.51e-01;		
Matches	6;	Conservative	1;	Mismatches 1; Indels 0; Gaps 0;

DB	75	LGKHLNSM	82
Oy	1	LGKHLNSM	8

RESULT	ID	SP	PRELIMINARY	PRT	513 AA
AC	063289				
DT	01-NOV-1996	(TREMBLREL. 01, CREATED)			
DT	01-NOV-1996	(TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1996	(TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DE	L1 RETROPOSON, ORF2 MRNA (PARTIAL) (FRAGMENT)				
OS	RATTUS NORVEGICUS (RAT)				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; RODENTIA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-LIVER:				
RX	MEDLINE: 92375092.				
RA	ILVES H., KAHR O., SPECK M.;				

Thu Jul 30 13:38:23 1998

US-08-817-547A-9.rspt

Page 2

RL MOL. CELL. BIOL. 12:4242-4248(1992).
DR EMBL: X61295; G56322; .
FT NON TER 1
SQ SEQUENCE 513 AA; 60414 MW; 3EB70B62 CRC32;

Query Match 83.1%; Score 49; DB 10; Length 513;
Best Local Similarity 75.0%; Pred. NO. 4.51e-01;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 423 IGRHLEHM 430
|||:|
OY 1 IGRHLSM 8

Search completed: Thu Jul 30 10:16:53 1998
Job time : 21 secs.

WIDEORH (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:20:02 1998; MasPar time 2.67 Seconds
40.289 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-10
Description: (1-7) from US08817547A.pep
Perfect Score: 51
Sequence: 1 GKHLSNM 7

Scoring table:
PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 14.516; Variance 40.392; scale 0.359

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of chance being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	51	100.0	27	3	P82185	Sequence of parathyro
2	51	100.0	34	22	W17939	Human parathyroid hor
3	51	100.0	34	22	W17954	Human parathyroid hor
4	51	100.0	34	22	W17955	Human parathyroid hor
5	51	100.0	34	22	W17950	Human PTH analogue [C
6	51	100.0	34	7	R34355	Human parathyroid hor
7	51	100.0	34	22	W17962	Human PTH analogue [C
8	51	100.0	34	22	W17951	Human parathyroid hor
9	51	100.0	34	19	R98951	Target peptide (PTH(1
10	51	100.0	34	22	W17943	Human parathyroid hor
11	51	100.0	34	22	W17944	Human parathyroid hor
12	51	100.0	34	22	W17947	Human parathyroid hor
13	51	100.0	36	9	R58243	Properlyl-[Al]-hPTH(1
14	51	100.0	36	9	R58177	[Morpholine-2-carboxy
15	51	100.0	36	9	R58170	[Nval]-hPTH(1-36)-NH
16	51	100.0	36	9	R58267	[Phe8]-hPTH(1-36)-NH
17	51	100.0	36	9	R58268	[Cha8]-hPTH(1-36)-NH
18	51	100.0	36	9	R58229	[Ala30]-hPTH(1-36)-NH
19	51	100.0	36	9	R58026	N-alpha-methyl[Ala1]

20	51	100.0	37	9	R58244	[Ala0]-hPTH(1-36)-NH	1.10e+01
21	51	100.0	38	9	R58141	[Leu21]-hPTH(1-38)-OH	1.10e+01
22	51	100.0	38	9	R58145	[Gly22]-hPTH(1-38)-OH	1.10e+01
23	51	100.0	38	9	R58075	[Ser33]-hPTH(1-38)-OH	1.10e+01
24	51	100.0	38	9	R58078	[Gly33]-hPTH(1-38)-OH	1.10e+01
25	51	100.0	38	19	R98958	Target peptide (PTH(1	1.10e+01
26	51	100.0	38	9	R58128	[Met19]-hPTH(1-38)-OH	1.10e+01
27	51	100.0	44	26	P30015	Human parathyroid hor	1.10e+01
28	51	100.0	47	25	W21946	Fusion protein compri	1.10e+01
29	51	100.0	84	27	W25687	Human parathyroid hor	1.10e+01
30	51	100.0	84	4	R21180	Human parathyroid hor	1.10e+01
31	51	100.0	84	4	R21181	Human parathyroid hor	1.10e+01
32	51	100.0	84	4	R21220	Human parathyroid hor	1.10e+01
33	51	100.0	84	4	R23226	Human parathyroid hor	1.10e+01
34	51	100.0	84	4	R23523	Human parathyroid hor	1.10e+01
35	51	100.0	84	7	R34460	Human parathyroid hor	1.10e+01
36	51	100.0	84	4	R21227	Human parathyroid hor	1.10e+01
37	51	100.0	84	4	R21226	Human parathyroid hor	1.10e+01
38	51	100.0	84	25	W29420	Human parathyroid hor	1.10e+01
39	51	100.0	84	4	R23229	Human parathyroid hor	1.10e+01
40	51	100.0	84	4	R23243	Human parathyroid hor	1.10e+01
41	51	100.0	84	4	R21197	Human parathyroid hor	1.10e+01
42	51	100.0	84	4	R23237	Human parathyroid hor	1.10e+01
43	51	100.0	84	4	R21218	Human parathyroid hor	1.10e+01
44	51	100.0	84	4	R21219	Human parathyroid hor	1.10e+01
45	51	100.0	84	9	R49694	Sequence of variant o	1.10e+01

ALIGNMENTS

RESULT 1
ID P82185 standard; Protein; 27 AA.

AC P82185;
DT 06-MAR-1992 (first entry)
DE Sequence of parathyroid hormone (PTH) analogue [L-Phe23]hPTH(7-34)NH2.
KW Parathyroid hormone analogue; osteoporosis therapy; hypercalcaemia;
KM hyperparathyroidism; hormone dependent tumour; bioassay; diagnosis;
KN treatment.
OS Homo sapiens.
PN US4771124-A.
PD 13-SEP-1988.
PF 26-MAY-1987; 054359.
PR 26-MAY-1987; US-054359.
PA (MERT) MERCK & CO INC.
PI Rosenblatt M, Caporale LH, Nutt RF, Levy JJ, Chorev M;
DR WPI: 88-278169/39.
PT Parathyroid hormone peptide analogues - used for treating
PT osteoporosis, hypercalcaemia, hyperparathyroidism and hormone
PT dependent tumours, and in vitro for bioassays
PS Clam 5; column 8; 5pp; English.
CC The PTH analogues of the invention are used for inhibiting the
CC naturally-occurring hormone in vivo and in vitro. They have high
CC binding affinity for their resp. cell surface receptors while not
CC stimulating prodn. of second messenger molecules. They may be used
CC in vitro in a bioassay for PTH and in vivo for therapy and diagnosis.
CC They are prepd. in dosage forms for oral, parenteral, rectal, intra-
CC nasal or topical admin.
SQ Sequence 27 AA;

Query Match 100.0%; Score 51; DB 3; Length 27;
Best local Similarity 100.0%; Pred. No. 1.10e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 gkhlsnm 12
QY 1 GKHLSNM 7

RESULT 2
ID W17939 standard; peptide; 34 AA.
AC W17939;
DT 29-JUL-1997 (first entry)
DE Human parathyroid hormone analogue [Cha7,11]hPTH(1-34)NH2.

KM Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
 KW bone fracture.
 OS Homo sapiens.
 OS Synthetic.
 FH Key
 FT modified_site 7 Location/Qualifiers
 FT /label= OTHER
 FT /note= "Cyclohexylalanine (Cha)"
 FT modified_site 11
 FT /label= OTHER
 FT /note= "Cha"
 FT modified_site 34
 FT /note= "In amide form"
 PN WO9702834-A1.
 PD 30-JAN-1997.
 PE 03-JUL-1996; U11292.
 PR 13-JUL-1995; US-001105.
 PR 06-SEP-1995; US-003305.
 PR 29-MAR-1996; US-626186.
 PR (BIOM-) BIOMEASURE INC.
 DONG ZX;
 WPI; 97-118819/11.
 PT New variants of human parathyroid hormone 1-34 peptide - which
 PT stimulate bone growth and are used for treatment of osteoporosis and
 PT bone fracture.
 PS Claim 5; Page -: 33pp; English.
 CC The present sequence is a specific example of a human parathyroid
 CC hormone (hPTH) analogue from fragment 1-34 in which at least one
 CC of the amino acid residues at positions 7, 11, 23, 24, 27, 28 and 31
 CC is cyclohexylalanine (Cha). In this example the Leu residue at
 CC position 7 and the Leu at position 11 in the wild-type have been
 CC substituted by Cha. The hPTH analogues stimulate bone growth and so
 CC are useful in human or veterinary medicine for treatment of
 CC osteoporosis and bone fracture, optionally in conjunction with
 CC anti-resorptive therapy (bisphosphonates and calcitonin).
 CC N.B. The present sequence does not appear in the specification. It
 CC corresponds to the known hPTH 1-34 fragment with the modifications
 CC as stated in the claim.
 SQ Sequence 34 AA;

Query Match 100.0%; Score 51; DB 22; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.10e+01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 gkhlnsm 18
 |||||
 QY 1 GKHLNSM 7

Search completed: Thu Jul 30 10:20:20 1998
 Job time : 18 secs.

W P E E L I
(TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:19:17 1998; Maspar time 3.25 Seconds
Tabular output not generated. 78.689 Million cell updates/sec

Title: >US-08-817-547A-10
Description: (1-7) from US08817547A.pep
Perfect Score: 51
Sequence: 1 GKHLNSM 7

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr56
1:plr1 2:plr2 3:plr3 4:plr4 5:nrl3d

Statistics: Mean 19.845; Variance 21.817; scale 0.910

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	51	100.0	34	5	12WA	parathyroid hormone (8.41e-02
2	51	100.0	34	5	12WE	parathyroid hormone (8.41e-02
3	51	100.0	34	5	12WG	parathyroid hormone 4 8.41e-02
4	51	100.0	34	5	12WF	parathyroid hormone 4 8.41e-02
5	51	100.0	35	5	12WD	parathyroid hormone (8.41e-02
6	51	100.0	36	5	12WB	parathyroid hormone (8.41e-02
7	51	100.0	37	5	12WB	parathyroid hormone (8.41e-02
8	51	100.0	37	5	12WB	parathyroid hormone (8.41e-02
9	51	100.0	37	5	12WB	parathyroid hormone (8.41e-02
10	47	92.2	115	2	JC4202	parathyroid hormone (8.32e-01
11	47	92.2	115	1	PTBO	parathyroid hormone p 8.32e-01
12	47	92.2	115	1	PTBO	parathyroid hormone p 8.32e-01
13	44	86.3	2105	1	A44059	RNA-directed RNA poly 4.31e+00
14	42	82.4	362	2	H69785	mannan endo-1,4-beta- 1.24e+01
15	42	82.4	363	2	H69393	iron-sulfur cluster b 1.24e+01
16	41	80.4	501	2	S45914	glucan 1,3-beta-glucos 1.24e+01
17	41	80.4	421	2	D69981	conserved hypotheticala 2.08e+01
18	41	80.4	513	2	S21976	probable RNA-directed 2.08e+01
19	41	80.4	558	2	S61604	probable membrane pro 2.08e+01
20	40	78.4	3005	2	S33642	homeotic protein zif- 2.45e+01
21	40	78.4	115	1	PTPG	parathyroid hormone p 3.45e+01
22	40	78.4	690	2	A24545	orf2 protein - Junon1 3.45e+01
23	39	76.5	176	2	I84638	triacylglycerol lipas 5.67e+01

24	39	76.5	263	2	B69807	polysaccharide deacet 5.67e+01
25	39	76.5	318	2	F38886	CoI Intron 13 protein 5.67e+01
26	39	76.5	356	2	S39889	SM1 protein - Podosp 5.67e+01
27	39	76.5	377	2	S61892	outer membrane protei 5.67e+01
28	39	76.5	437	2	S52014	atp6 protein - common 5.67e+01
29	39	76.5	437	2	S48853	H++transporting ATP s 5.67e+01
30	39	76.5	587	2	S61038	D-lactate dehydrogena 5.67e+01
31	39	76.5	648	2	A61617	cycK protein homolog 5.67e+01
32	39	76.5	662	2	S61193	probable membrane pro 5.67e+01
33	38	74.5	152	2	S22311	HMG-Y-related protein 9.24e+01
34	38	74.5	176	2	S22310	HMG-Y-related protein 9.24e+01
35	38	74.5	181	2	A64393	hypothetical protein 9.24e+01
36	38	74.5	193	2	A53835	SEC63 protein complex 9.24e+01
37	38	74.5	290	2	A36134	REPA protein - Escher 9.24e+01
38	38	74.5	545	2	E69907	DNA recombinase homol 9.24e+01
39	38	74.5	670	2	S47042	protein kinase (EC 2. 9.24e+01
40	37	72.5	193	2	E69469	hypothetical protein 1.49e+02
41	37	72.5	253	1	PMHUYM	phosphoglycerate muta 1.49e+02
42	37	72.5	295	5	2AT2A	aspartate transcarbam 1.49e+02
43	37	72.5	295	5	2AT2B	aspartate transcarbam 1.49e+02
44	37	72.5	295	5	2AT2C	aspartate transcarbam 1.49e+02
45	37	72.5	491	2	I40991	signal transducer amp 1.49e+02

ALIGNMENTS

RESULT	1	12WA	#type complete
ENTRY		parathyroid hormone (residues 1-34) - human	
TITLE		HPTH(1-34)	
ALTERNATE_NAMES		Structure of human parathyroid hormone fragment 1-34, NMR 10	
PDB-TITLE		Structure of human parathyroid hormone fragment 1-34, NMR 10	
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67856	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-References		PDB:12WA	
REFERENCE		TN001717	
#authors		Marx, U.C.	
#book		In Strukturen Verschiedener Parathormonfragmente In Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996	
COMMENT		Resolution: not applicable	
KEYWORDS		Determination: NMR	
FEATURE		hormone	
FEATURE		6-9	
SUMMARY		#region helix (right hand alpha) \	
		#region helix (right hand alpha)	
		#length 34 #molecular-weight 4118 #checksum 5629	
Query Match		100.0%; Score 51; DB 5; Length 34;	
Best Local Similarity		100.0%; Pred. No. 8.41e-02;	
Matches		7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
DB	12	GKHLNSM 18	
QY	1	GKHLNSM 7	
RESULT	2	12WE	#type complete
ENTRY		parathyroid hormone (residues 4-37) - human	
TITLE		HPTH(4-37)	
ALTERNATE_NAMES		Structure of human parathyroid hormone fragment 4-37, NMR 10	
PDB-TITLE		Structure of human parathyroid hormone fragment 4-37, NMR 10	
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67860	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-References		PDB:12WE	
REFERENCE		TN001721	
#authors		Marx, U.C.	
#book		In Strukturen Verschiedener Parathormonfragmente In Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996	

COMMENT Resolution: not applicable
 COMMENT Determination: NMR
 KEYWORDS hormone
 FEATURE 15-25
 SUMMARY

#region helix (right hand alpha)
 #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 51; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 8.41e-02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 GKHLNSM 15
 QY 1 GKHLNSM 7

Search completed: Thu Jul 30 10:19:45 1998
 Job time : 28 secs.

RP REVISIONS.
 RX MEDLINE; 75146516.
 RA KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL BIOCHEMISTRY 14:1842-1847(1975).
 [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE; 75059220.
 RA TREGGAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D.,
 RA KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL HOPE-SEYLER S. Z. PHYSIOL. CHEM. 355:415-421(1974).
 [9]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE; 73227467.
 RA ANDREKITA R.H., HARTMANN A., JOEHL A., KAMBER B., MAIER R.,
 RA KLINKER B., RITTEL W., SIEBER P.;
 RL HELV. CHIM. ACTA 56:470-473(1973).
 [10]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE; 91299748.
 RA KLAUS W., DIECKMANN T., WRAY V., SCHOMBURG D., WINGENDER E., MAYER H.;
 RL BIOCHEMISTRY 30:6936-6942(1991).
 [11]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE; 93345518.
 RA BARDEEN J.A., CUTHBERTSON R.M.;
 RL EUR. J. BIOCHEM. 215:315-321(1993).
 [12]
 RP STRUCTURE BY NMR OF 32-68.
 RX MEDLINE; 95318084.
 RA MARX U.C., AUSTERMANN S., BAYER P., ADERMAN K., ECHART A.,
 RA STICHT H., WALTER S., SCHMID F.-X., JAEHNICKE R., FORSSMANN W.-G.,
 RA ROESCH P.;
 RL J. BIOL. CHEM. 270:15194-15202(1995).
 [13]
 RP VARIANT ARG-18.
 RX MEDLINE; 91009811.
 RA ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,
 RA KRONENBERG H.M.;
 RL J. CLIN. INVEST. 86:1084-1087(1990).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
 CC HYPOPARATHYROIDISM (FHH).
 CC EMBL; J00301; G190704; -.
 DR EMBL; V000597; G37144; -.
 DR EMBL; A29146; E186700; -.
 DR PIR; A01536; PTHU.
 DR PIR; A19339; A19339.
 PDB; 1HPH; 10-JUL-95.
 PDB; 1HTH; 15-OCT-97.
 PDB; 12WA; 12-MAR-97.
 PDB; 12WB; 12-MAR-97.
 PDB; 12WC; 12-MAR-97.
 PDB; 12WD; 12-MAR-97.
 PDB; 12WE; 12-MAR-97.
 PDB; 12WF; 16-JUN-97.
 PDB; 12WG; 16-JUN-97.
 DR MIM; 146200; -.
 DR MIM; 168450; -.
 DR PROSITE; PS00335; PARATHYROID; 1.
 KW HORMONE; SIGNAL; DISEASE MUTATION; 3D-STRUCTURE.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT VARIANT 18 18
 FT CONFLICT 107 107
 FT SEQUENCE 115 AA; 12861 MW; 243887C7 CRC32;
 N -> D (IN REF. 5).
 C -> R (IN FHH; LEADS TO INEFFICIENT
 PROCESSING OF THE PRECURSOR).
 Query Match 100.0%; Score 51; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 7.72e-03;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 43 GKHLNSM 49
 QY 1 GKHLNSM 7
 RESULT 2
 ID PTH1_BOVIN STANDARD; PRT; 115 AA.
 AC P01268;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
 GN PTH.
 OS BOS TAURUS (BOVINE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHIRIA; ARTIODACTYLA.
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 80056617.
 RA KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
 RA POTTS J.T. JR., RICH A.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 82037785.
 RA WEAVER C.A., GORDON D.F., KEMPER B.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 83105964.
 RA WEAVER C.A., GORDON D.F., KEMPER B.;
 RL MOL. CELL. ENDOCRINOL. 28:411-424(1982).
 [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 84262483.
 RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
 RL GENE 28:319-322(1984).
 [5]
 RP SEQUENCE OF 26-115.
 RX MEDLINE; 74142666.
 RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,
 RA COHN D.V.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
 [6]
 RP SEQUENCE OF 32-115.
 RX MEDLINE; 71076162.
 RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,
 RA AURBACH G.D., POTTS J.T. JR.;
 RL HOPE-SEYLER S. Z. PHYSIOL. CHEM. 351:1586-1588(1970).
 [7]
 RP SEQUENCE OF 32-115.
 RX MEDLINE; 71063634.
 RA BREWER H.B. JR., RONAN R.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
 [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE; 71091588.
 RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
 RA DEFLOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC EMBL; V00106; G85; -.
 DR EMBL; J00023; G163641; -.
 DR EMBL; J00024; G163643; -.
 DR EMBL; J00024; E18249; ALT_SEQ.
 DR EMBL; J00024; E18250; ALT_SEQ.
 DR EMBL; K01938; G163647; -.
 DR EMBL; M25082; G163645; -.
 DR PIR; A01536; PTHO.
 DR PIR; A24945; A24949.
 DR PROSITE; PS00335; PARATHYROID; 1.
 KW HORMONE; SIGNAL.

W E S E R F H
(TM)

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Search_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:18:13 1998; Maspar time 3.99 Seconds
73.877 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-10
Description: (1-7) from US08817547A.pep
Perfect Score: 51
Sequence: 1 GKHLNSM 7

Scoring table:
PAM 150
Gap 15

Searched: 140542 seqs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptemb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 19.774; Variance 18.165; scale 1.089

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	43	84.3	719	3	017828	COBF8.2.	1.84e+00
2	42	82.4	362	9	005512	BACILLUS SP. MANNAN EN	3.42e+00
3	42	82.4	363	9	029112	IRON-SULFUR CLUSTER BI	3.42e+00
4	41	80.4	75	7	038347	ORF75.	6.31e+00
5	41	80.4	367	10	063728	HYPOHETICAL 43.7 KD P	6.31e+00
6	41	80.4	421	9	034528	RYVN PROTEIN.	6.31e+00
7	41	80.4	513	10	063289	LI RETROPOSON, ORF2 MR	6.31e+00
8	41	80.4	1072	2	015101	ZINC FINGER HOMEODOMAI	6.31e+00
9	41	80.4	1300	10	P97692	LI RETROTRANSPOSON ORF	6.31e+00
10	41	80.4	3703	2	015911	ZINC FINGER HOMEODOMAI	6.31e+00
11	41	80.4	3726	10	061329	AT MOTIF BINDING FACTO	6.31e+00
12	40	78.4	545	11	090054	ORF2.	1.15e+01
13	39	76.5	39	11	065545	EBV B95-8 CC(E) DNA WI	2.07e+01
14	39	76.5	143	7	003935	MINOR CAPSID PROTEIN.	2.07e+01
15	39	76.5	242	3	018238	Y57G11C.14.	2.07e+01
16	39	76.5	263	9	034928	YFUS PROTEIN.	2.07e+01
17	39	76.5	318	6	002684	HYPOHETICAL 36.5 KD P	2.07e+01
18	39	76.5	437	6	036379	ATP SYNTHASE A CHAIN (2.07e+01
19	39	76.5	643	3	022010	R186.4.	2.07e+01
20	39	76.5	3429	3	024593	X GENE.	2.07e+01

21	38	74.5	181	9	058155	HYPOTHETICAL 21.1 KD P	3.69e+01
22	38	74.5	290	9	003086	REPLICATION PROTEIN A	3.69e+01
23	38	74.5	315	3	021593	HYPOTHETICAL 36.4 KD P	3.69e+01
24	38	74.5	367	9	045125	MOBILIZATION PROTEIN.	3.69e+01
25	38	74.5	439	8	041770	ALPHA-AMYLASE.	3.69e+01
26	38	74.5	472	3	009656	HYPOTHETICAL 52.6 KD P	3.69e+01
27	38	74.5	545	9	032006	YOKA PROTEIN.	3.69e+01
28	38	74.5	686	3	P92006	CATALASE (EC 1.11.1.6)	3.69e+01
29	38	74.5	711	9	P95539	CDG2-RELATED PROTEIN K	3.69e+01
30	38	74.5	719	3	025826	HYPOTHETICAL 140.5 KD	3.69e+01
31	38	74.5	1258	3	010908	SIMILARITY TO MULTIPLE	3.69e+01
32	38	74.5	1372	3	P91526	UVRB (FRAGMENT).	6.49e+01
33	37	72.5	95	9	053074	PARATHYROID HORMONE (F	6.49e+01
34	37	72.5	105	10	063473	HYPOTHETICAL 22.0 KD P	6.49e+01
35	37	72.5	193	9	028516	PUTATIVE - POSSIBLE PH	6.49e+01
36	37	72.5	196	9	006737	SULFIDE-DEHYDROGENASE	6.49e+01
37	37	72.5	247	9	007821	HYPOTHETICAL PROTEIN.	6.49e+01
38	37	72.5	258	8	023434	CHROMOSOME XV READING	6.49e+01
39	37	72.5	271	1	008558	PROSAPOSIN.	6.49e+01
40	37	72.5	518	12	013035	CHITINASE.	6.49e+01
41	37	72.5	573	11	010621	G3R PROTEIN.	6.49e+01
42	37	72.5	585	11	007041	NUCLEOSIDE TRIPHOSPHAT	6.49e+01
43	37	72.5	940	1	007048	RNA POLYMERASE (FRAGME	6.49e+01
44	37	72.5	940	1	007048	RNA POLYMERASE (FRAGME	6.49e+01
45	37	72.5	1371	2	015067	KIAA0361 (FRAGMENT).	6.49e+01

ALIGNMENTS

RESULT 1	PRELIMINARY: PRT: 719 AA.
ID 017828;	
AC 017828;	
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)	
DI 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)	
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)	
DE COBF8.2.	
OS CAENORHABDITIS ELEGANS.	
OC EUKARYOTA; METAZOA; ACCELONATES; NEMATODA; SECERNENTEA; RHABDITIDA.	
RN [1]	
RP SEQUENCE FROM N.A.	
RA HARRIS B.;	
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.	
RN [2]	
RP SEQUENCE FROM N.A.	
RX MEDLINE; 94150718.	
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,	
RA BONFIELD J., BURTON J., CONNELL M., COPEY T., COOPER J., COULSON A.,	
RA CRATON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,	
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,	
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,	
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,	
RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SANDERS D., SHOWNKEEN R.,	
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,	
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;	
RL NATURE 368:32-38(1994).	
DR EMBL; 273103; E242596;	
SO SEQUENCE 719 AA; 81009 MW; E206BB38 CRC32;	
Query Match	84.3%; Score 43; DB 3; Length 719;
Best Local Similarity	71.4%; Pred. No. 1.84e+00;
Matches	5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
DB 637 SKHLSM 643	
QY 1 GKHLNSM 7	
RESULT 2	PRELIMINARY: PRT: 362 AA.
ID 005512;	
AC 005512;	
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)	
DI 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)	

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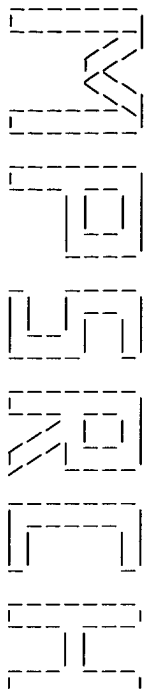
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE BACILLUS SP. MANNAN ENDO-1.
GN YDHT.
OS BACILLUS SUBTILIS.
OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-168.
RA SADAE Y., YATA K., FUJITA M., SAGAI H., ITAYA M., KASAHARA Y.,
RA Ogasawara N.,
RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-168.
RA SADAE Y., YATA K., FUJITA M., SAGAI H., ITAYA M., KASAHARA Y.,
RA Ogasawara N.,
RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-168.
RA KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
RA BORRIS R., BOURSIER L., BRANS A., BRAUN M., BRIGHELL S.C., BRON S.,
RA BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
RA DENIZOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMERSON P.T.,
RA ENITAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOUGER D.,
RA FRITZ C., FUJITA M., FUJITA Y., FUMA S., GALIZZI A., GALLERON N.,
RA GHIM S.Y., GLASER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G.,
RA GIUSEPPI G., GUY B.J., HAGA K., HALECH J., HARWOOD C.R., HENAUT A.,
RA HILBERT H., HOLSAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L.,
RA JORIS B., KARAMATA D., KASAHARA Y., KLAERR-BLANCHARD M., KLEIN C.,
RA KOBAYASHI Y., KOETTER P., KONIGSTEIN G., KROGH S., KUMANO M.,
RA KURITA K., LAPIDUS A., LARDINOIS S., LAUBER J., LAZAREVIC V.,
RA LEE S.M., LEVINE A., LIU H., MASUDA S., MAUEL C., MEDIGUE C.,
RA MEDINA N., MELIADO R.P., MIZUNO M., MOESTL D., NAKAI S., NOBACK M.,
RA NOONE D., O'REILLY M., OGAMA K., OGIMARA A., OUDEGA B., PARK S.H.,
RA PARO V., POHL T.M., PORTELELL D., FORNOLIK S., PRESCOTT A.M.,
RA PRESECAN E., PUJIC P., PURNELLE B., RAPOPORT G., REY M., REYNOLDS S.,
RA RIEGER M., RIYOLTA C., ROCHA E., ROCHE B., ROSE M., SADAE Y.,
RA SATO T., SCANLAN E., SCHLEICH S., SCHROETER R., SCOPFONE F.,
RA SERIGUCHI J., SEROWSKA A., SEROR S.J., SEROR P., SHIN B.S., SOLDO B.,
RA SOROKIN A., TACCONI E., TAKAGI T., TAKAHASHI H., TAKEMARU K.,
RA TAKUCHI M., TAMAKOSHI A., TANAKA T., TERPSTRA P., TOGNONI A.,
RA TOSATO V., UCHIYAMA S., VANDENBOL M., VANNIE F., VASSAROTTI A.,
RA VIARI A., WAMBUT R., WEDLER E., WEDLER H., WEITZENGGER T.,
RA WINTERS P., WIPAR A., YAMAMOTO H., YAMANE K., YASUMOTO K., YATA K.,
RA YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A.,
RA NATURE 390:249-256(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-168.
RA KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.,
RA SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: D88802; D1020491; -.
DR EMBL: 299107; E1182567; -.
SQ SEQUENCE 362 AA; 40834 MW; 616962F9 CRC32;

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Query Match 82.4%; Score 42; DB 9; Length 362;
Best Local Similarity 71.4%; Pred. No. 3.42e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 162 GKRLNAM 168
QY 1 GKRLNSM 7

Search completed: Thu Jul 30 10:18:58 1998
Job time : 45 secs.



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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:22:22 1998; MasPar time 2.66 Seconds
34.605 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-11
Description: (1-6) from US08817547A.pep
Perfect Score: 44
Sequence: 1 KHLNSM 6

Scoring table: PAM 150
Gap 15

Searched: 124785 segs, 15338987 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 13.509; Variance 37.219; scale 0.363

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	44	100.0	34	22	W17968	Human parathyroid hor	4.47e+01
2	44	100.0	34	22	W17939	Human parathyroid hor	4.47e+01
3	44	100.0	34	22	W17935	Human parathyroid hor	4.47e+01
4	44	100.0	34	22	W17954	Human parathyroid hor	4.47e+01
5	44	100.0	34	22	W17969	Human parathyroid hor	4.47e+01
6	44	100.0	34	22	W17951	Human parathyroid hor	4.47e+01
7	44	100.0	34	8	R41537	[Gln25,26,27]hPTH (1-	4.47e+01
8	44	100.0	34	19	R89951	Target peptide (PTH(1-	4.47e+01
9	44	100.0	34	9	R58016	N-alpha-isopropyl-hPT	4.47e+01
10	44	100.0	34	22	W17943	Human parathyroid hor	4.47e+01
11	44	100.0	34	22	W17944	Human parathyroid hor	4.47e+01
12	44	100.0	34	22	W17947	Human parathyroid hor	4.47e+01
13	44	100.0	36	9	R58262	[Ala1]-hPTH(1-36)-NH	4.47e+01
14	44	100.0	36	9	R58026	N-alpha-methyl[Ala1]	4.47e+01
15	44	100.0	36	9	R58243	Propargyl-[Ala1]-hPTH	4.47e+01
16	44	100.0	36	9	R58267	[Phe8]-hPTH(1-36)-NH	4.47e+01
17	44	100.0	36	9	R58268	[Cha8]-hPTH(1-36)-NH	4.47e+01
18	44	100.0	36	9	R58230	[D-Val31]-hPTH(1-36)-	4.47e+01
19	44	100.0	37	9	R58244	[Ala0]-hPTH(1-36)-NH	4.47e+01

20	44	100.0	38	9	R58141	[Leu21]-hPTH(1-38)-OH	4.47e+01
21	44	100.0	38	9	R58147	[His22]-hPTH(1-38)-OH	4.47e+01
22	44	100.0	38	9	R58128	[Met19]-hPTH(1-38)-OH	4.47e+01
23	44	100.0	38	9	R58132	[Pro19]-hPTH(1-38)-OH	4.47e+01
24	44	100.0	38	19	R98958	Target peptide (PTH(1	4.47e+01
25	44	100.0	44	26	P30015	Human parathyroid hor	4.47e+01
26	44	100.0	47	25	W21946	Fusion protein compit	4.47e+01
27	44	100.0	78	6	R30859	Leu8 hPTH (7-84) mute	4.47e+01
28	44	100.0	81	6	R30854	hPTH mutein lacking 3	4.47e+01
29	44	100.0	84	27	W25687	Human parathyroid hor	4.47e+01
30	44	100.0	84	27	R21210	Human parathyroid hor	4.47e+01
31	44	100.0	84	4	R23526	Human parathyroid hor	4.47e+01
32	44	100.0	84	4	R23525	Human parathyroid hor	4.47e+01
33	44	100.0	84	4	R23235	Human parathyroid hor	4.47e+01
34	44	100.0	84	4	R23523	Human parathyroid hor	4.47e+01
35	44	100.0	84	4	R21209	Human parathyroid hor	4.47e+01
36	44	100.0	84	25	W29420	Human parathyroid hor	4.47e+01
37	44	100.0	84	4	R21253	Human parathyroid hor	4.47e+01
38	44	100.0	84	4	R21161	Human parathyroid hor	4.47e+01
39	44	100.0	84	4	R21160	Human parathyroid hor	4.47e+01
40	44	100.0	84	4	R21236	Human parathyroid hor	4.47e+01
41	44	100.0	84	4	R21254	Human parathyroid hor	4.47e+01
42	44	100.0	84	4	R21218	Human parathyroid hor	4.47e+01
43	44	100.0	84	4	R23227	Human parathyroid hor	4.47e+01
44	44	100.0	84	4	R23231	Human parathyroid hor	4.47e+01
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ALIGNMENTS

RESULT 1
ID W17968 standard; peptide; 34 AA.
AC W17968;
DT 29-JUL-1997 (first entry)
DE Human parathyroid hormone analogue [N631]hPTH(1-34)NH2.
KW Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
KM bone fracture.
OS Homo sapiens.
FH Synthetic.
FT modified_site 31 Location/Qualifiers
FT modified_site 34 /label= Nle
FT modified_site 34 /note= "In amide form"
FT FT
FN WO9702834-A1.
PD 30-JAN-1997.
PF 03-JUL-1996: U11292.
PR 13-JUL-1995: US-001105.
PR 06-SEP-1995: US-003305.
PR 29-MAR-1996: US-626186.
PA (BIOM-) BIOMEASURE INC.
PI Dong ZX;
DR WPI: 97-118819/11.
PT New variants of human parathyroid hormone 1-34 peptide - which
PT stimulate bone growth and are used for treatment of osteoporosis and
PT bone fracture
PS Claim 20: Page -: 33pp: English.
CC The present sequence is a specific example of a human parathyroid
CC hormone (hPTH) analogue from fragment 1-34 in which at least the amino
CC acid residue at position 1 is alpha, beta-diaminopropionic acid,
CC the amino acid residue at position 27 is homocysteine, or the amino acid
CC residue at position 31 is norleucine. In this example the Val residue at
CC position 31 in the wild-type has been substituted by Nle. The hPTH
CC analogue stimulate bone growth and so are useful in human or
CC veterinary medicine for treatment of osteoporosis and bone fracture,
CC optionally in conjunction with anti-resorptive therapy (bisphosphonates
CC and calcitonin).
CC N.B. The present sequence does not appear in the specification. It
CC corresponds to the known hPTH 1-34 fragment with the modifications
CC as stated in the claim.
SQ Sequence 34 AA;
Query Match 100.0%; Score 44; DB 22; Length 34;

Best Local Similarity 100.0%; Pred. No. 4.47e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 13 khlnsm 18
| | | | |
QY 1 KHLNSM 6

RESULT 2

ID W17939 standard; peptide; 34 AA.
AC W17939;
DT 29-JUL-1997 (first entry)
DE Human parathyroid hormone analogue [Cha7,11]hPTH(1-34)NH2.
KW Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
KW bone fracture.
OS Homo sapiens.
OS Synthetic.

FH Key Location/Qualifiers
FT modified_site 7 /label= OTHER

FT modified_site 11 /note= "Cyclohexylalanine (Cha)"
FT /label= OTHER
FT /note= "Cha"

FT modified_site 34 /note= "in amide form"

FN W09702834-A1.
PN 30-JAN-1997.

PF 03-JUL-1996; U11292.

PR 13-JUL-1995; US-001105.

PR 06-SEP-1995; US-003305.

PR 29-MAR-1996; US-626186.

PA (BIOM-) BIOMESURE INC.

PI Dong ZX.

DR WPI; 97-118819/11.

PT New variants of human parathyroid hormone 1-34 peptide - which

stimulate bone growth and are used for treatment of osteoporosis and

bone fracture

PS Claim 5; Page -: 33pp; English.

CC The present sequence is a specific example of a human parathyroid

hormone (hPTH) analogue from fragment 1-34 in which at least one

of the amino acid residues at positions 7, 11, 23, 24, 27, 28 and 31

is cyclohexylalanine (Cha). In this example the leu residue at

position 7 and the leu at position 11 in the wild-type have been

substituted by Cha. The hPTH analogues stimulate bone growth and so

are useful in human or veterinary medicine for treatment of

osteoporosis and bone fracture, optionally in conjunction with

anti-resorptive therapy (bisphosphonates and calcitonin).

N.B. The present sequence does not appear in the specification. It

corresponds to the known hPTH 1-34 fragment with the modifications

as stated in the claim.

SC Sequence 34 AA;

Query Match 100.0%; Score 44; DB 22; Length 34;

Best Local Similarity 100.0%; Pred. No. 4.47e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 13 khlnsm 18
| | | | |
QY 1 KHLNSM 6

Search completed: Thu Jul 30 10:22:35 1998
Job time : 13 secs.

W D S E I F
(TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:21:36 1998; Maspar time 3.04 Seconds
Tabular output not generated. 72.203 Million cell updates/sec

Title: >US-08-817-547A-11
Description: (1-6) from US08817547A.pep
Perfect Score: 44
Sequence: 1 KHLNSM 6

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr56
1:plr1 2:plr2 3:plr3 4:plr4 5:nrl3d

Statistics: Mean 18.883; Variance 20.866; scale 0.905

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	44	100.0	34	5 1ZWA	parathyroid hormone (2.07e+00	
2	44	100.0	34	5 1ZWE	parathyroid hormone (2.07e+00	
3	44	100.0	34	5 1ZWF	parathyroid hormone 4 2.07e+00	
4	44	100.0	34	5 1ZWD	parathyroid hormone (2.07e+00	
5	44	100.0	36	5 1ZWB	parathyroid hormone (2.07e+00	
6	44	100.0	37	5 1ZPB	parathyroid hormone (2.07e+00	
7	44	100.0	37	5 1ZPH	parathyroid hormone (2.07e+00	
8	44	100.0	115	1 PTHU	parathyroid hormone P 2.07e+00	
9	44	100.0	2105	1 A44059	RNA-directed RNA poly 2.07e+00	
10	41	93.2	3005	2 S33642	homeotic protein zfh- 1.05e+01	
11	40	90.9	37	5 1ZWC	parathyroid hormone (1.77e+01	
12	40	90.9	115	2 JCA202	parathyroid hormone (1.77e+01	
13	40	90.9	115	1 PTHO	parathyroid hormone P 1.77e+01	
14	40	90.9	421	2 D69981	conserved hypothetical 2.97e+01	
15	39	88.6	662	2 S61193	probable membrane pro 4.93e+01	
16	38	86.4	545	2 E69907	DNA recombinase homol 8.09e+01	
17	37	84.1	193	2 E69469	hypothetical protein 8.09e+01	
18	37	84.1	196	2 C69839	phospho-adenylsulfa 8.09e+01	
19	37	84.1	208	2 D65041	hypothetical protein 8.09e+01	
20	37	84.1	247	2 S72904	phosphoglycerate muta 8.09e+01	
21	37	84.1	253	1 PMHUYM	phosphoglycerate muta 8.09e+01	
22	37	84.1	253	1 PMRTYM	phosphoglycerate muta 8.09e+01	
23	37	84.1	271	2 S67072	probable membrane pro 8.09e+01	

24	37	84.1	295	5	2AT2A	Aspartate transcarbam 8.09e+01
25	37	84.1 <td>295<td>5<th>2AT2B</th><th>Aspartate transcarbam 8.09e+01</th></td></td>	295 <td>5<th>2AT2B</th><th>Aspartate transcarbam 8.09e+01</th></td>	5 <th>2AT2B</th> <th>Aspartate transcarbam 8.09e+01</th>	2AT2B	Aspartate transcarbam 8.09e+01
26	37	84.1 <td>295<td>5<th>2AT2C</th><th>Aspartate transcarbam 8.09e+01</th></td></td>	295 <td>5<th>2AT2C</th><th>Aspartate transcarbam 8.09e+01</th></td>	5 <th>2AT2C</th> <th>Aspartate transcarbam 8.09e+01</th>	2AT2C	Aspartate transcarbam 8.09e+01
27	37	84.1 <td>304<td>1<th>OWBSAC</th><th>aspartate carbamoyl tr 8.09e+01</th></td></td>	304 <td>1<th>OWBSAC</th><th>aspartate carbamoyl tr 8.09e+01</th></td>	1 <th>OWBSAC</th> <th>aspartate carbamoyl tr 8.09e+01</th>	OWBSAC	aspartate carbamoyl tr 8.09e+01
28	37	84.1 <td>384<td>2<th>S73429</th><th>glycerol-3-phosphate d 8.09e+01</th></td></td>	384 <td>2<th>S73429</th><th>glycerol-3-phosphate d 8.09e+01</th></td>	2 <th>S73429</th> <th>glycerol-3-phosphate d 8.09e+01</th>	S73429	glycerol-3-phosphate d 8.09e+01
29	37	84.1 <td>430<td>2<th>A65165</th><th>protein dfr - Escheri 8.09e+01</th></td></td>	430 <td>2<th>A65165</th><th>protein dfr - Escheri 8.09e+01</th></td>	2 <th>A65165</th> <th>protein dfr - Escheri 8.09e+01</th>	A65165	protein dfr - Escheri 8.09e+01
30	37	84.1 <td>438<td>2<th>A64147</th><th>hypothetical protein 8.09e+01</th></td></td>	438 <td>2<th>A64147</th><th>hypothetical protein 8.09e+01</th></td>	2 <th>A64147</th> <th>hypothetical protein 8.09e+01</th>	A64147	hypothetical protein 8.09e+01
31	37	84.1 <td>491<td>2<th>I40990</th><th>signal transducer amp 8.09e+01</th></td></td>	491 <td>2<th>I40990</th><th>signal transducer amp 8.09e+01</th></td>	2 <th>I40990</th> <th>signal transducer amp 8.09e+01</th>	I40990	signal transducer amp 8.09e+01
32	37	84.1 <td>491<td>2<th>I40991</th><th>signal transducer amp 8.09e+01</th></td></td>	491 <td>2<th>I40991</th><th>signal transducer amp 8.09e+01</th></td>	2 <th>I40991</th> <th>signal transducer amp 8.09e+01</th>	I40991	signal transducer amp 8.09e+01
33	37	84.1 <td>491<td>2<th>I40989</th><th>signal transducer amp 8.09e+01</th></td></td>	491 <td>2<th>I40989</th><th>signal transducer amp 8.09e+01</th></td>	2 <th>I40989</th> <th>signal transducer amp 8.09e+01</th>	I40989	signal transducer amp 8.09e+01
34	37	84.1 <td>491<td>2<th>S37391</th><th>amg protein - Escher 8.09e+01</th></td></td>	491 <td>2<th>S37391</th><th>amg protein - Escher 8.09e+01</th></td>	2 <th>S37391</th> <th>amg protein - Escher 8.09e+01</th>	S37391	amg protein - Escher 8.09e+01
35	37	84.1 <td>585<td>2<th>C36858</th><th>G3R protein - variola 8.09e+01</th></td></td>	585 <td>2<th>C36858</th><th>G3R protein - variola 8.09e+01</th></td>	2 <th>C36858</th> <th>G3R protein - variola 8.09e+01</th>	C36858	G3R protein - variola 8.09e+01
36	37	84.1 <td>648<td>1<th>NPVZCP</th><th>nucleoside-triphospha 8.09e+01</th></td></td>	648 <td>1<th>NPVZCP</th><th>nucleoside-triphospha 8.09e+01</th></td>	1 <th>NPVZCP</th> <th>nucleoside-triphospha 8.09e+01</th>	NPVZCP	nucleoside-triphospha 8.09e+01
37	37	84.1 <td>648<td>1<th>NPVZAM</th><th>nucleoside-triphospha 8.09e+01</th></td></td>	648 <td>1<th>NPVZAM</th><th>nucleoside-triphospha 8.09e+01</th></td>	1 <th>NPVZAM</th> <th>nucleoside-triphospha 8.09e+01</th>	NPVZAM	nucleoside-triphospha 8.09e+01
38	37	84.1 <td>700<td>2<th>S12053</th><th>protein-tyrosine-phos 8.09e+01</th></td></td>	700 <td>2<th>S12053</th><th>protein-tyrosine-phos 8.09e+01</th></td>	2 <th>S12053</th> <th>protein-tyrosine-phos 8.09e+01</th>	S12053	protein-tyrosine-phos 8.09e+01
39	37	84.1 <td>931<td>2<th>G69615</th><th>Arp-dependent DNA hel 8.09e+01</th></td></td>	931 <td>2<th>G69615</th><th>Arp-dependent DNA hel 8.09e+01</th></td>	2 <th>G69615</th> <th>Arp-dependent DNA hel 8.09e+01</th>	G69615	Arp-dependent DNA hel 8.09e+01
40	37	84.1 <td>1101<td>2<th>S51823</th><th>myosin heavy chain AT 8.09e+01</th></td></td>	1101 <td>2<th>S51823</th><th>myosin heavy chain AT 8.09e+01</th></td>	2 <th>S51823</th> <th>myosin heavy chain AT 8.09e+01</th>	S51823	myosin heavy chain AT 8.09e+01
41	36	81.8 <td>101<td>2<th>S64056</th><th>probable membrane pro 1.32e+02</th></td></td>	101 <td>2<th>S64056</th><th>probable membrane pro 1.32e+02</th></td>	2 <th>S64056</th> <th>probable membrane pro 1.32e+02</th>	S64056	probable membrane pro 1.32e+02
42	36	81.8 <td>142<td>2<th>S04071</th><th>hemoglobin alpha chal 1.32e+02</th></td></td>	142 <td>2<th>S04071</th><th>hemoglobin alpha chal 1.32e+02</th></td>	2 <th>S04071</th> <th>hemoglobin alpha chal 1.32e+02</th>	S04071	hemoglobin alpha chal 1.32e+02
43	36	81.8 <td>511<td>2<th>JC1404</th><th>CD81-box DNA-binding 1.32e+02</th></td></td>	511 <td>2<th>JC1404</th><th>CD81-box DNA-binding 1.32e+02</th></td>	2 <th>JC1404</th> <th>CD81-box DNA-binding 1.32e+02</th>	JC1404	CD81-box DNA-binding 1.32e+02
44	36	81.8 <td>587<td>2<th>H64045</th><th>msbA protein - Haemop 1.32e+02</th></td></td>	587 <td>2<th>H64045</th><th>msbA protein - Haemop 1.32e+02</th></td>	2 <th>H64045</th> <th>msbA protein - Haemop 1.32e+02</th>	H64045	msbA protein - Haemop 1.32e+02
45	36	81.8 <td>922<td>2<th>S31164</th><th>Arp-dependent ClpB pr 1.32e+02</th></td></td>	922 <td>2<th>S31164</th><th>Arp-dependent ClpB pr 1.32e+02</th></td>	2 <th>S31164</th> <th>Arp-dependent ClpB pr 1.32e+02</th>	S31164	Arp-dependent ClpB pr 1.32e+02

ALIGNMENTS

RESULT	1	1ZWA	#type complete
ENTRY		parathyroid hormone (residues 1-34) - human	
TITLE		PTH(1-34)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 1-34, NMR 10	
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ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67856	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		TN001717	
REFERENCE		TN001717	
#book		Marx, U.C.	
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FEATURE		determination: NMR	
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		#region helix (right hand alpha)	
		#length 34 #molecular-weight 4118 #checksum 5629	
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DB	13 KHLNSM	18	
Oy	1 KHLNSM	6	
RESULT	2	1ZWE	#type complete
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TITLE		PTH(4-37)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 4-37, NMR 10	
PDB-TITLE		structures	
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REFERENCE		A67860	
#authors		Roesch, P.; Marx, U.C.	
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#cross-references		TN001721	
REFERENCE		TN001721	
#book		Marx, U.C.	
		In Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996	

COMMENT Resolution: not applicable
 COMMENT Determination: NMR
 KEYWORDS hormone
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 SUMMARY #region helix (right hand alpha)
 #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 44; DB 5; Length 34;
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 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 KHLNSM 15
 QY 1 KHLNSM 6

Search completed: Thu Jul 30 10:22:04 1998
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RP REVISIONS.
 RX MEDLINE; 75146516.
 RA KEUTMANN H.T., NIALI H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL BIOCHEMISTRY 14:1842-1847(1975).
 RN [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE; 75059220.
 RA TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALI H.D.,
 RA KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL HOPE-SEYLER S.Z. PHYSIOL. CHEM. 355:415-421(1974).
 RN [9]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE; 73227467.
 RA ANDREATA R.H., HARTMANN A., JOEHL A., KAMBER B., MAIER R.,
 RA KRIEGER B., RITTEL W., SIEBER P.;
 RL HELV. CHIM. ACTA 56:470-473(1973).
 RN [10]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE; 91299748.
 RA KLAUS W., DIECKMANN T., WRAY V., SCHOMBURG D., WINGENDER E., MAYER H.;
 RL BIOCHEMISTRY 30:6936-6942(1991).
 RN [11]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE; 93345518.
 RA BARDEEN J.A., CUTHBERTSON R.M.;
 RL EUR. J. BIOCHEM. 215:315-321(1993).
 RN [12]
 RP STRUCTURE BY NMR OF 32-68.
 RX MEDLINE; 95318084.
 RA MARK U.C., AUSTERMANN S., BAYER P., ADERMAN K., ECHART A.,
 RA STICHT H., WALTER S., SCHMID F.-X., JENICKE R., FORSMANN W.-G.,
 RA ROESCH P.;
 RL J. BIOL. CHEM. 270:15194-15202(1995).
 RN [13]
 RP VARIANT ARG-18.
 RX MEDLINE; 91009811.
 RA ANNOUD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,
 RA KRONENBERG H.M.;
 RL J. CLIN. INVEST. 86:1084-1087(1990).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
 CC HYPOPARATHYROIDISM (PTH).
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 DR EMBL; V00597; G37144; -.
 DR EMBL; A29146; E186700; -.
 DR PIR; A01536; PTHU.
 DR PIR; A19339; A19339.
 DR PDB; 1HRH; 10-JUL-95.
 DR PDB; 1HTH; 15-OCT-97.
 DR PDB; 1ZWA; 12-MAR-97.
 DR PDB; 1ZWB; 12-MAR-97.
 DR PDB; 1ZWC; 12-MAR-97.
 DR PDB; 1ZWD; 12-MAR-97.
 DR PDB; 1ZWE; 12-MAR-97.
 DR PDB; 1ZNF; 16-JUN-97.
 DR PDB; 1ZNG; 16-JUN-97.
 DR MIM; 146200; -.
 DR MIM; 168450; -.
 DR PROSITE; PS00335; PARATHYROID; 1.
 DR KM HORMONE; SIGNAL; DISEASE MUTATION; 3D-STRUCTURE.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT VARIANT 18 18
 FT CONFLICT 107 107
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 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 44 KHLNSM 49
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 QY 1 KHLNSM 6
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 AC P36309;
 DT 01-JUN-1994 (REL. 29, CREATED)
 DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE GENOME POLYPROTEIN (CONTAINS: RNA REPLICASE (EC 2.7.7.48); HELICASE;
 DE COAT PROTEIN).
 OS APPLE STEM GROOVING VIRUS (STRAIN P-209) (ASGV).
 OC VIRIDAE; SS-RNA NONENVELOPED VIRUSES; CAPILLIVIRIDAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93033164.
 RA YOSHIKAWA N., SASAKI E., KATO M., TAKAHASHI T.;
 RL VIROLOGY 191:98-105(1992).
 CC -1- PTH: THE N-TERMINAL OF THE COAT PROTEIN IS BLOCKED.
 CC -1- THE COAT PROTEIN IS LOCATED IN THE CARBOXY-TERMINAL REGION OF
 CC THIS POLYPROTEIN.
 DR EMBL; D14995; G285608; -.
 DR PIR; A44059; A44059.
 DR RNA-DIRECTED RNA POLYMERASE; POLYPROTEIN; ATP-BINDING; COAT PROTEIN;
 KW HELICASE.
 FT NP_BIND 781 788
 FT DOMAIN 1364 1453
 FT SEQUENCE 2105 AA; 241240 MM; B3EE0CC2C CRC32;
 SQ
 Query Match 100.0%; Score 44; DB 1; Length 2105;
 Best Local Similarity 100.0%; Pred. No. 3.21e-01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1794 KHLNSM 1799
 |||||
 QY 1 KHLNSM 6

Search completed: Thu Jul 30 10:20:44 1998
 Job time : 7 secs.

W O R L D
(TM)

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Msrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:21:01 1998; Maspar time 3.61 seconds
Tabular output not generated. 69.980 Million cell updates/sec

Title: >US-08-817-547A-11
Description: (1-6) from US08817547A.pep
Perfect Score: 44
Sequence: 1 KHLNSM 6

Scoring table:
PAM 150
Gap 15

Searched: 140542 seqs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptemb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 18.888; Variance 17.056; scale 1.107

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	42	95.5	719	3	017828	COB8.2.	1.30e+00
2	41	93.2	1072	2	015101	ZINC FINGER HOMEODOMAI	2.48e+00
3	41	93.2	3703	2	015111	ZINC FINGER HOMEODOMAI	2.48e+00
4	41	93.2	3726	10	061329	AT MOTIF BINDING FACTO	2.48e+00
5	40	90.9	421	9	034528	YRAN PROTEIN.	4.68e+00
6	38	86.4	315	3	021593	HYPOHETICAL 36.4 KD P	1.60e+01
7	38	86.4	367	9	045125	MOBILIZATION PROTEIN.	1.60e+01
8	38	86.4	545	9	032006	YOKA PROTEIN.	1.60e+01
9	38	86.4	666	3	P92006	MO4G12.3.	1.60e+01
10	38	86.4	711	9	P95539	CATALASE (EC 1.11.1.6)	1.60e+01
11	37	84.1	133	4	029256	UNKNOWN PROTEIN (FRAGM	2.91e+01
12	37	84.1	193	9	028516	HYPOHETICAL 22.0 KD P	2.91e+01
13	37	84.1	193	9	053772	TRANSPOSON TNS405 AND	2.91e+01
14	37	84.1	196	9	006737	PUTATIVE - POSSIBLE PH	2.91e+01
15	37	84.1	258	6	035690	COXI INTRON 1 ORF.	2.91e+01
16	37	84.1	271	1	008558	CHROMOSOME XV READING	2.91e+01
17	37	84.1	439	8	041770	ALPHA-AmyLASE.	2.91e+01
18	37	84.1	491	8	096275	MCN2-RELATED PROTEIN (2.91e+01
19	37	84.1	518	12	013035	PROSAPOSTIN.	2.91e+01
20	37	84.1	554	3	023651	ZK863.3.	2.91e+01

ALIGNMENTS

RESULT	ID	1	PRELIMINARY:	PRT:	719 AA.
AC	017828				
DT	01-NOV-1996	(TREMBLREL. 01, CREATED)			
DT	01-NOV-1996	(TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1996	(TREMBLREL. 01, LAST ANNOTATION UPDATE)			
DE	COB8.2..	CAENORHABDITIS ELEGANS.			
OS	CAENORHABDITIS ELEGANS.				
OC	EUKARYOTA; METAZOA; ACCELONATES; NEMATODA; SECERNENTERA; RHABDITIDA.				
RN	[1]	SEQUENCE FROM N.A.			
RP	HARRIS B.				
RL	SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.				
RN	[2]	SEQUENCE FROM N.A.			
RP	MEDLINE; 94150718.				
RX	WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,				
RA	BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,				
RA	CRATON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,				
RA	GARDNER A., GREEN P., HAWKINS J., KIRSTEN J., LAISTER N., LATREILLE P.,				
RA	JONES M., KERSHAW J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,				
RA	LIGHTNING J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,				
RA	PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,				
RA	SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULLIVAN J.,				
RA	THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,				
RA	WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,				
RL	NATURE 368:32-38(1994).				
DR	EMBL; 273103; E242596; .				
SQ	SEQUENCE 719 AA; 81009 MW; E206BB38 CRC32;				
Query Match		95.5%;	Score 42;	DB 3;	Length 719;
Best Local Similarity		83.3%;	Pred. No. 1.30e+00;		
Matches	5;	Conservative	1;	Mismatches	0;
Indels	0;	Gaps	0;		
DB	638 KHLNSM 643				
QY	1 KHLNSM 6				
RESULT	2	PRELIMINARY:	PRT:	1072 AA.	
ID	015101				
AC	015101				
DT	01-JAN-1998	(TREMBLREL. 05, CREATED)			
DT	01-JAN-1998	(TREMBLREL. 05, LAST SEQUENCE UPDATE)			

DT 01-JAN-1998 (TREMERE). 05, LAST ANNOTATION UPDATE)
 DE ZINC FINGER HOMEODOMAIN PROTEIN (3' PARTIAL) (FRAGMENT).
 GN A-418G10.1.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUKARYOTA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA ADAMS M.D., LOFTUS B.J., ZHOU L., LABOMBARD M., FUHRMANN J.,
 RA BRADON R., KIM U.J., KERLAVAGE A.R., VENTER J.C.;
 RL SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AC002044; G2347080; -
 KW HOMEODOMAIN; DNA-BINDING; NUCLEAR PROTEIN.
 FT NON_TER 1072 1072
 SQ SEQUENCE 1072 AA; 115896 MW; 78611913 CRC32;

Query Match
 Best Local Similarity 93.2%; Score 41; DB 2; Length 1072;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 749 KHLNNM 754
 QY 1 KHLNSM 6

Search completed: Thu Jul 30 10:21:19 1998
 Job time : 18 secs.

Db 8 hlsm 12
|||||
QY 1 HLNSM 5

RESULT 2
ID P40427 standard; peptide; 32 AA.
AC P40427;
DT 22-JUL-1992 (first entry)
DE Parathyroid antagonist peptide.
KW Human thyroid hormone.
OS Homo sapiens.
FH Key Location/Qualifiers
FT misc_difference 32 /note= "Phe or Tyr"
FT J59042351-A.
PN 08-MAR-1984.
PF 1-SEP-1982; 150702.
PF 01-SEP-1982; JP-150702.
PF (TOXN) TOYO JOZO KK.
PF WPI; 84-097433/16.
PT h-PTH Peptide (3-34) derivatives - are N-terminal fragments of human
PT thyroid hormone
PS Claim 1. Page 1; 25pp; Japanese.
CC The peptide is an N-terminal fragment deriv. of human thyroid
CC hormone (amino acids 3-34) and is an antagonist of parathyroid
CC hormone. It is expected to be a therapeutic agent of hyperfunction
CC of accessory thyroid.
SQ Sequence 32 AA;

Query Match 100.0%; Score 37; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.89e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 12 hlsm 16
|||||
QY 1 HLNSM 5

Search completed: Thu Jul 30 10:24:56 1998
Job time : 11 secs.

W I S E N E I F (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:24:01 1998; Maspar time 3.08 Seconds
Tabular output not generated. 59.270 Million cell updates/sec

Title: >US-08-817-547A-12
Description: (1-5) from US08817547A.pep
Perfect Score: 37
Sequence: 1 HLNSM 5

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr56
1:plrl 2:plrl2 3:plrl3 4:plrl4 5:nlrl3d

Statistics: Mean 17.600; Variance 17.971; scale 0.979

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	37	100.0	34	5 1ZWA	parathyroid hormone (1.96e+01	
2	37	100.0	34	5 1ZWE	parathyroid hormone (1.96e+01	
3	37	100.0	34	5 1ZMG	parathyroid hormone 4 (1.96e+01	
4	37	100.0	34	5 1ZWF	parathyroid hormone 4 (1.96e+01	
5	37	100.0	35	5 1ZWD	parathyroid hormone (1.96e+01	
6	37	100.0	36	5 1ZWB	parathyroid hormone (1.96e+01	
7	37	100.0	37	5 1HPH	parathyroid hormone f (1.96e+01	
8	37	100.0	115	1 PTHU	parathyroid hormone p (1.96e+01	
9	37	100.0	193	2 E69469	hypothetical protein (1.96e+01	
10	37	100.0	208	2 D65041	hypothetical protein (1.96e+01	
11	37	100.0	384	2 S73429	glycerol-3-phosphate d (1.96e+01	
12	37	100.0	385	2 C36858	G3R protein - variola (1.96e+01	
13	37	100.0	2105	1 A44059	RNA-directed RNA poly (1.96e+01	
14	35	94.6	186	2 H64785	hypothetical protein (5.87e+01	
15	35	94.6	216	2 C64622	osmoprotection protei (5.87e+01	
16	35	94.6	369	2 S74983	hypothetical protein (5.87e+01	
17	35	94.6	389	2 UC5136	naringenin-chalcone s (5.87e+01	
18	35	94.6	396	2 S20515	naringenin-chalcone s (5.87e+01	
19	35	94.6	398	2 S58190	naringenin-chalcone s (5.87e+01	
20	35	94.6	410	2 S12224	naringenin-chalcone s (5.87e+01	
21	35	94.6	419	2 S74500	zeaxanthin glucosyl t (5.87e+01	
22	35	94.6	423	2 T64063	histidine--tRNA ligas (5.87e+01	
23	35	94.6	500	2 S50508	ANP1 protein - yeast (5.87e+01	

24	35	94.6	587	2 S61038	D-lactate dehydrogena (5.87e+01
25	35	94.6	662	2 S61193	probable membrane pro (5.87e+01
26	35	94.6	684	2 B69308	conserved hypotheticala (5.87e+01
27	35	94.6	696	2 A65130	hypothetical 79.5 kd (5.87e+01
28	35	94.6	880	2 S49627	regulatory protein AR (5.87e+01
29	35	94.6	922	2 S31164	AMP-dependent cIpb pr (5.87e+01
30	35	94.6	1642	2 S11018	cobra venom factor pr (5.87e+01
31	35	94.6	3411	1 GNMVYP	genome polypotein - (5.87e+01
32	35	94.6	3411	1 GNMVYP	genome polypotein - (5.87e+01
33	34	91.9	151	2 F69986	acetyltransferase hom (9.99e+01
34	34	91.9	154	2 J00860	hypothetical 18k prot (9.99e+01
35	34	91.9	232	2 S72439	GIP cyclonhydrolase I (9.99e+01
36	34	91.9	317	2 I52575	gene NRK protein - mo (9.99e+01
37	34	91.9	346	2 S62197	molymbdenum formylmeth (9.99e+01
38	34	91.9	354	2 JC1366	tyrosine kinase recep (9.99e+01
39	34	91.9	396	1 R3BYML	ribosomal protein var (9.99e+01
40	34	91.9	447	2 C64828	hypothetical protein (9.99e+01
41	34	91.9	593	2 A47186	receptor protein tyro (9.99e+01
42	34	91.9	594	2 I66248	receptor tyrosine kin (9.99e+01
43	34	91.9	594	2 I58386	receptor tyrosine kin (9.99e+01
44	34	91.9	607	2 I37560	protein-tyrosine kin (9.99e+01
45	34	91.9	3005	2 S33642	homeotic protein zfh-

ALIGNMENTS

RESULT	1	1ZWA	#type complete
ENTRY		parathyroid hormone (residues 1-34) - human	
TITLE		HPTH(1-34)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 1-34, NMR 10	
PDB_TITLE		structure of human parathyroid hormone fragment 1-34, NMR 10	
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67856	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:1ZWA	
REFERENCE		TN001717	
#authors		Marx, U.C.	
#book		in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996	
COMMENT		Resolution: not applicable	
COMMENT		Determination: NMR	
KEYWORDS		hormone	
FEATURE			
6-9		#region helix (right hand alpha)\	
19-30		#region helix (right hand alpha)	
SUMMARY		#length 34 #molecular-weight 4118 #checksum 5629	
Query Match		100.0%; Score 37; DB 5; Length 34;	
Best Local Similarity		100.0%; Pred. No. 1.96e+01;	
Matches		5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
DB	14	HLNSM 18	
QY	1	HLNSM 5	
RESULT	2	1ZWE	#type complete
ENTRY		parathyroid hormone (residues 4-37) - human	
TITLE		HPTH(4-37)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 4-37, NMR 10	
PDB_TITLE		structure of human parathyroid hormone fragment 4-37, NMR 10	
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67860	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:1ZWE	
REFERENCE		TN001721	
#authors		Marx, U.C.	
#book		in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996	

COMMENT Resolution: not applicable
COMMENT Determination: NMR
KEYWORDS hormone
FEATURE
15-25
SUMMARY #region helix (right hand alpha)
#length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 37; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.96e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

DB 11 HLNSM 15
QY 1 HLNSM 5

Search completed: Thu Jul 30 10:24:27 1998
Job time : 26 secs.

WISSE (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:22:54 1998; Maspar time 2.01 Seconds
62,468 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-12
Description: (1-5) from US08817547A.pep
Perfect Score: 37
Sequence: 1 HLNSM 5

Scoring table:
Gap 15
PAM 150

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: wisw-prot35
1:swiss1

Statistics: Mean 18.404; Variance 15.219; scale 1.209

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	37	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	5.14e+00
2	37	100.0	208	1	YFJY_ECOLI HYPOTHETICAL 24.6 KD P	5.14e+00
3	37	100.0	384	1	Y039_MYCPN HYPOTHETICAL PROTEIN M	5.14e+00
4	37	100.0	692	1	YI13_CAEEL PROBABLE G. PROTEIN-COU	5.14e+00
5	37	100.0	2105	1	POLR_ASGVP GENOME POLYPROTEIN (CN	5.14e+00
6	35	94.6	389	1	CHS2_LYCES CHALCONE SYNTHASE 2 (E	1.85e+01
7	35	94.6	396	1	CHSY_PINSY CHALCONE SYNTHASE (EC	1.85e+01
8	35	94.6	398	1	CHSY_ORYSA CHALCONE SYNTHASE (EC	1.85e+01
9	35	94.6	422	1	SYH_HABIN HISTIDYL-TRNA SYNTHETA	1.85e+01
10	35	94.6	500	1	ANPL_YEAST AMINONITROPHENYL PROPA	1.85e+01
11	35	94.6	587	1	DLDI_YEAST D-LACTATE DEHYDROGENAS	1.85e+01
12	35	94.6	662	1	PMT7_YEAST DOLICHYL-PHOSPHATE-MAN	1.85e+01
13	35	94.6	696	1	YHFK_ECOLI HYPOTHETICAL 79.5 KD P	1.85e+01
14	35	94.6	859	1	Y0D3_CAEEL HYPOTHETICAL 96.7 KD P	1.85e+01
15	35	94.6	880	1	ARG2_YEAST ARGININE METABOLISM RE	1.85e+01
16	35	94.6	922	1	CLPA_PEA ATP-DEPENDENT CLP PROT	1.85e+01
17	35	94.6	3411	1	POLG_YEFAV GENOME POLYPROTEIN (CO	1.85e+01
18	35	94.6	3411	1	POLG_YEFAV GENOME POLYPROTEIN (CO	1.85e+01
19	34	91.9	154	1	YR7E_ECOLI HYPOTHETICAL 18.0 KD P	3.44e+01
20	34	91.9	325	1	YK84_CAEEL HYPOTHETICAL 28.1 KD P	3.44e+01
21	34	91.9	339	1	RMAR_CANGA MITOCHONDRIAL RIBOSOMA	3.44e+01
22	34	91.9	355	1	DYR1_BRARE DYR-1 PROTEIN PRECURSO	3.44e+01
23	34	91.9	396	1	RMAR_YEAST MITOCHONDRIAL RIBOSOMA	3.44e+01

RESULT	ID	PTHY_HUMAN	STANDARD	PRT	115 AA.	ALIGNMENTS
AC	21-JUL-1986	(REL. 01, CREATED)				
DT	13-AUG-1987	(REL. 05, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).					
GN	PTH.					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
OC	EUTHERIA; PRIMATES.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	MEDLINE: 82150870.					
RA	HENDY G.N., KRONENBERG H.M., POTTS J.T., JR., RICH A.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RA	MEDLINE: 83169834.					
RA	VASICER T.J., MCCREYTT B.E., FREEMAN M.W., FENNICK B.J.;					
RA	HENDY G.N., POTTS J.T., JR., RICH A., KRONENBERG H.M.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 80:2127-2131(1983).					
RN	[3]					
RP	SEQUENCE OF 26-37.					
RA	MEDLINE: 74174967.					
RA	JACOBS J.W., KEMPER B., NIALL H.D., HABENER J.F., POTTS J.T., JR.;					
RL	NATURE 249:155-157(1974).					
RN	[4]					
RP	SEQUENCE OF 32-68.					
RA	MEDLINE: 7411656.					
RA	NIALL H.D., SAUER R.T., JACOBS J.W., KEUTMANN H.T., SEGRE G.V.;					
RA	O'RIORDAN J.L.H., AUBACH G.D., POTTS J.T., JR.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).					
RN	[5]					
RP	SEQUENCE OF 61-83 AND 84-115.					
RA	MEDLINE: 79082855.					
RA	KEUTMANN H.T., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.;					
RA	POTTS J.T., JR.;					
RL	BIOCHEMISTRY 17:5723-5729(1978).					
RN	[6]					
RP	SEQUENCE OF 75-100.					
RA	KEUTMANN H.T., NIALL H.D., JACOBS J.W., BARLING P.M., HENDY G.N.;					
RA	O'RIORDAN J.L.H., POTTS J.T., JR.;					
RL	(IN) CALCULUM-REGULATING HORMONES, TALMADE R.V., OWEN M.;					
RL	PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM,					
RL	(1975).					
RN	[7]					

RP REVISIONS.
 RX MEDLINE: 75146516.
 RA KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL BIOCHEMISTRY 14:1842-1847(1975).
 RN [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 75059220.
 RA TREGGAR G.W., VAN RIENSCHOTEN J., GREEN E., NIALL H.D.,
 RA KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL HOPE-SEYLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
 RN [9]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 73227467.
 RA ANDREATA R.H., HARTMANN A., JOEHL A., KAMBER B., MALER R.,
 RA RINIER B., RITTEL W., SIEBER P.;
 RL HELV. CHIM. ACTA 56:470-473(1973).
 RN [10]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE: 91298748.
 RA KLAUS W., DIECKMANN T., WRAY V., SCHOMBURG D., WINGENDER E., MAYER H.;
 RL BIOCHEMISTRY 30:6936-6942(1991).
 RN [11]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE: 93345518.
 RA BARDEN J.A., CUTHBERTSON R.M.;
 RL EUR. J. BIOCHEM. 215:315-321(1993).
 RN [12]
 RP STRUCTURE BY NMR OF 32-68.
 RX MEDLINE: 95318084.
 RA MAX U.C., AUSTERMANN S., BAYER P., ADERMAN K., ECHART A.,
 RA STICHT H., WALTER S., SCHMID F.-X., JAEHNCKE R., FORSMANN W.-G.,
 RL ROSCH P.;
 RN J. BIOL. CHEM. 270:15194-15202(1995).
 RN [13]
 RP VARIANT ARG-18.
 RX MEDLINE: 91009811.
 RA ARNOOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,
 RA KRONENBERG H.M.;
 RL J. CLIN. INVEST. 86:1084-1087(1990).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
 CC HYPOPARATHYROIDISM (FTH).
 DR EMBL: J00301: G180704; -.
 DR EMBL: V00597: G37144; -.
 DR EMBL: A29146: E186700; -.
 DR PIR: A01536; PTHU.
 DR PIR: A19339; A19339.
 DR PDB: 1HPH: 10-JUL-95.
 DR PDB: 1HTH: 15-OCT-97.
 DR PDB: 12WA: 12-MAR-97.
 DR PDB: 12WB: 12-MAR-97.
 DR PDB: 12WC: 12-MAR-97.
 DR PDB: 12WD: 12-MAR-97.
 DR PDB: 12WE: 12-MAR-97.
 DR PDB: 12WF: 16-JUN-97.
 DR PDB: 12WG: 16-JUN-97.
 DR MIM: 146200; -.
 DR MIM: 168450; -.
 DR PROSITE: PS00335; PARATHYROID, 1.
 DR KW HORMONE; SIGNAL; DISEASE MUTATION; 3D-STRUCTURE.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT VARIANT 18 18
 FT CONFLICT 107 107 PARATHYROID HORMONE.
 FT SEQUENCE 115 AA; 12861 MM; 24388/7 CRC32; C -> R (IN FTH; LEADS TO INEFFICIENT
 N -> D (IN REF. 5)).
 Query Match 100.0%; Score 37; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 5.14e+00;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 45 HLNSM 49
 QY 1 HLNSM 5
 RESULT 2
 ID YFJU_ECOLI STANDARD; PRT; 208 AA.
 AC P52125;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 24.6 KD PROTEIN IN ALPA-GABD INTERGENIC REGION (0208).
 GN YFJU.
 OS ESCHERICHIA COLI.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC ENTEROBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RA BRATTNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
 RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- SIMILARITY: STRONG, TO E.COLI YAKG.
 DR EMBL: U36840; G1033121; -.
 DR EMBL: AE000348; G1768979; -.
 DR ECOGENE: EG13196; YFJU.
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 208 AA; 24560 MM; B33D5203 CRC32;
 Query Match 100.0%; Score 37; DB 1; Length 208;
 Best Local Similarity 100.0%; Pred. No. 5.14e+00;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 29 HLNSM 33
 QY 1 HLNSM 5

Search completed: Thu Jul 30 10:23:01 1998
 Job time : 7 secs.

 MIPSEIN (TM)

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Mparch_p protein - protein database search, using Smith-Waterman algorithm
 on: Thu Jul 30 10:23:18 1998; MasPar time 3.59 Seconds
 58.637 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-817-547A-12
 Description: (1-5) from US08817547A.pep
 Perfect Score: 37
 Sequence: 1 HLN5M 5

Scoring table: PAM 150
 Gap 15

Searched: 140542 seqs, 42109429 residues
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: sptemb15
 1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
 5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
 9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
 13:sp_unclassified

Statistics: Mean 17.650; Variance 14.986; scale 1.178

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	37	100.0	133	4	Q29256	UNKNOWN PROTEIN (FRAGM 6.33e+00
2	37	100.0	193	9	Q28516	HYPOTHETICAL 22.0 KD P 6.33e+00
3	37	100.0	193	9	Q53772	TRANSPOSON TNS405 AND 6.33e+00
4	37	100.0	258	6	Q35690	COXI INTRON 1 ORF. 6.33e+00
5	37	100.0	585	11	Q07041	G3R PROTEIN. 6.33e+00
6	37	100.0	585	11	Q89097	GARCIA-1966 RIGHT NEAR 6.33e+00
7	37	100.0	1354	3	Q23669	ZK930.1. 6.33e+00
8	37	100.0	3429	3	Q24593	X GENE. 6.33e+00
9	35	94.6	106	8	Q41051	PROLINE- AND LEUCINE-R 2.32e+01
10	35	94.6	186	9	P77528	FROM BASES 555801 TO 5 2.32e+01
11	35	94.6	207	8	Q41292	CHALCONE SYNTHASE (FRA 2.32e+01
12	35	94.6	216	9	Q25497	OSMOPROTECTION PROTEIN 2.32e+01
13	35	94.6	369	9	P73003	HYPOTHETICAL 39.0 KD P 2.32e+01
14	35	94.6	386	8	Q23923	CHALCONE SYNTHASE (FRA 2.32e+01
15	35	94.6	389	8	Q43188	CHALCONE SYNTHASE (EC 2.32e+01
16	35	94.6	398	8	P93710	CHALCONE SYNTHASE (EC 2.32e+01
17	35	94.6	419	9	P72650	ZEAXANTHIN GLUCOSYL TR 2.32e+01
18	35	94.6	472	3	Q09656	HYPOTHETICAL 52.6 KD P 2.32e+01
19	35	94.6	684	9	Q29784	CONSERVED HYPOTHETICAL 2.32e+01
20	35	94.6	719	3	Q17828	CO8F8.2. 2.32e+01

ALIGNMENTS

RESULT	ID	Q29256	PRELIMINARY	PRT	133 AA.
AC	Q29256				
DT	01-NOV-1996	(TREMBLREL. 01, CREATED)			
DT	01-NOV-1996	(TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-MAY-1997	(TREMBLREL. 03, LAST ANNOTATION UPDATE)			
DE	UNKNOWN PROTEIN (FRAGMENT).				
OS	SUS SCROFA (PIG).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; ARTIODACTYLA.				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=SMALL INTESTINE;				
RA	WINTEROE A.K., FREDHOLM M., DAVIES W.;				
RL	MAMM. GENOME 7:509-517(1996).				
DR	EMBL; F15072; G971974; --				
FT	NON_TER 1				
FT	NON_TER 133				
SO	SEQUENCE 133 AA; 14447 MW; 3C3E9163 CRC32;				
Query Match		100.0%;	Score 37;	DB 4;	Length 133;
Best Local Similarity		100.0%;	Pred. No. 6.33e+00;		
Matches	5;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
Db	3 HLN5M 7				
QY	1 HLN5M 5				
RESULT	2	PRELIMINARY;	PRT;	193 AA.	
ID	Q28516				
AC	Q28516				
DT	01-JAN-1998	(TREMBLREL. 05, CREATED)			
DT	01-JAN-1998	(TREMBLREL. 05, LAST SEQUENCE UPDATE)			
DT	01-JAN-1998	(TREMBLREL. 05, LAST ANNOTATION UPDATE)			
DE	HYPOTHETICAL 22.0 KD PROTEIN.				
GN	AF1758.				
OS	ARCHAEOGLOBUS FULIGINUS.				
OC	ARCHAEBACTERIA; EUDYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE.				
RP	SEQUENCE FROM N.A.				
RA	KLEIN H.P., CLAYTON R.A., TOMB J., WHITE O., KETCHUM K.A.,				
RA	DODSON R.J., GRINNIN M., HICKEY E.K., PETERSON J.D., RICHARDSON D.L.,				
RA	KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C., FLEISCHMANN R.D.,				

RA QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S., KIRKNESS E.F.,
 RA DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B., PETERSON S.,
 RA REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L., OVERBECK R.,
 RA GOCAYNE J.D., WEIDMAN J.F., McDONALD L., UTTERBACK T., COTTON M.D.,
 RA SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M., SADOW P.W.,
 RA D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., MASON T.M.,
 RA OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.,
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 (2)
 RP SEQUENCE FROM N.A.
 RA KLEBK H.P., CLAYTON R.A., TOMB J., WHITE O., NELSON K.E., KETCHUM K.A.,
 RA DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D., RICHARDSON D.L.,
 RA KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C., FLEISCHMANN R.D.,
 RA QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S., KIRKNESS E.F.,
 RA DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B., PETERSON S.,
 RA REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L., OVERBECK R.,
 RA GOCAYNE J.D., WEIDMAN J.F., McDONALD L., UTTERBACK T., COTTON M.D.,
 RA SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M., SADOW P.W.,
 RA D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., MASON T.M.,
 RA OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.,
 SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 EMBL, AEO00981, G2648792; -.
 KM HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 193 AA; 22041 MW; 59F1ED0E CRC32;

Query Match 100.0%; Score 37; DB 9; Length 193;
 Best local Similarity 100.0%; Pred. No. 6.33e+00;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 44 HLNSM 48
 QY 1 HLNSM 5

Search completed: Thu Jul 30 10:23:44 1998
 Job time : 26 secs.

WIDEORIT (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:27:11 1998; MasPar time 2.64 Seconds
52.320 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-13
Description: (1-9) from US08817547A.pep
Perfect Score: 62
Sequence: 1 HNLGKHLNS 9

Scoring table:
PAM 150
Gap 15

Searched: 124785 segs, 15338987 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 15.334; Variance 52.987; scale 0.289

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	62	100.0	34	9	R58181	[Thr33, Ala34]-hPTH(1-4.68e+00	
2	62	100.0	34	22	W17957	Human parathyroid hor 4.68e+00	
3	62	100.0	34	22	W17954	Human parathyroid hor 4.68e+00	
4	62	100.0	34	22	W17955	Human parathyroid hor 4.68e+00	
5	62	100.0	34	22	W17950	Human PTH analogue [C 4.68e+00	
6	62	100.0	34	22	W17969	Human parathyroid hor 4.68e+00	
7	62	100.0	34	22	W17970	Human PTH analogue [D 4.68e+00	
8	62	100.0	34	7	R34354	Human parathyroid hor 4.68e+00	
9	62	100.0	34	7	R34353	Human parathyroid hor 4.68e+00	
10	62	100.0	34	22	W17943	Human parathyroid hor 4.68e+00	
11	62	100.0	34	22	W17949	Human parathyroid hor 4.68e+00	
12	62	100.0	34	22	W17948	Human parathyroid hor 4.68e+00	
13	62	100.0	35	14	R74516	Parathyroid hormone p 4.68e+00	
14	62	100.0	35	14	R74517	Parathyroid hormone p 4.68e+00	
15	62	100.0	35	14	R74402	Parathyroid hormone p 4.68e+00	
16	62	100.0	35	14	R74401	Parathyroid hormone p 4.68e+00	
17	62	100.0	35	14	R74429	Parathyroid hormone p 4.68e+00	
18	62	100.0	35	14	R74431	Parathyroid hormone p 4.68e+00	
19	62	100.0	36	9	R58182	[Nval]-hPTH(1-36)-NH2 4.68e+00	

20	62	100.0	36	9	R58279	[Lys20]-hPTH(1-36)-NH 4.68e+00
21	62	100.0	36	9	R58177	[Morpholine-2-carboxy 4.68e+00
22	62	100.0	36	9	R58176	[Hexahydroxyindazole- 4.68e+00
23	62	100.0	36	9	R58248	N-Dimethyl-1-[Ala1]-hPT 4.68e+00
24	62	100.0	36	9	R58247	[Hyp1]-hPTH(1-36)-NH2 4.68e+00
25	62	100.0	36	2	R52395	Human parathyroid hor 4.68e+00
26	62	100.0	36	9	R58246	Acetyl-hPTH(1-36)-NH2 4.68e+00
27	62	100.0	36	9	R58242	[Lys(isopropyl)13]-hp 4.68e+00
28	62	100.0	36	9	R58175	[Pyridine-2-carboxyl 4.68e+00
29	62	100.0	36	9	R58295	[D-Val35]-hPTH(1-36)- 4.68e+00
30	62	100.0	38	9	R58164	[Asp33]-hPTH(1-38)-OH 4.68e+00
31	62	100.0	44	26	P30015	Human parathyroid hor 4.68e+00
32	62	100.0	47	25	W21946	Fusion protein compit 4.68e+00
33	62	100.0	84	27	W25687	Human parathyroid hor 4.68e+00
34	62	100.0	84	4	R21198	Human parathyroid hor 4.68e+00
35	62	100.0	84	4	R21199	Human parathyroid hor 4.68e+00
36	62	100.0	84	25	W29420	Human parathyroid hor 4.68e+00
37	62	100.0	84	4	R21153	Human parathyroid hor 4.68e+00
38	62	100.0	84	4	R21152	Human parathyroid hor 4.68e+00
39	62	100.0	84	6	R30851	Generic human parathy 4.68e+00
40	62	100.0	84	7	R34460	Human parathyroid hor 4.68e+00
41	62	100.0	84	4	R21250	Human parathyroid hor 4.68e+00
42	62	100.0	84	4	R21251	Human parathyroid hor 4.68e+00
43	62	100.0	84	4	R23245	Human parathyroid hor 4.68e+00
44	62	100.0	84	4	R23243	Human parathyroid hor 4.68e+00
45	62	100.0	229	9	R47971	Sequence of a full-le

ALIGNMENTS

RESULT 1
ID R58181 standard; peptide; 34 AA.

AC R58181;
DT 20-SEP-1994 (first entry)
DE [Thr33, Ala34]-hPTH(1-34)-NH2.
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_site 34 /note="in amide form"
FT
PV GB2269176-A.
PD 02-FEB-1994.
PE 12-JUL-1993; 014384.
PR 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (SANO) SANDOZ LTD.
PA (BAUER) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
PI Gilbert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Maelchli R, Rainer A;
DR WPI: 94-018352/03.
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 179; Page 43; 92pp; English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 34 AA;

Query Match 100.0%; Score 62; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.68e+00;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 hnlgkhlns 17
 QY 1 HNLGKHLNS 9

RESULT 2

ID W17957 standard; peptide: 34 AA.
 AC W17957;
 DT 29-JUL-1997 (first entry)
 DE Human parathyroid hormone analogue [Alb3]hPTH(1-34)NH2.
 KW Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
 OS bone fracture.
 OS Homo sapiens.
 OS Synthetic.
 FH Key
 FT modified_site 3 Location/Qualifiers
 FT modified_site 34 /label= Alb

modified_site 34 /note= "In amide form"

PD WO9702834-A1.
 PE 30-JAN-1997.
 PR 03-JUL-1996; U11292.
 PR 13-JUL-1995; US-001105.
 PR 06-SEP-1995; US-003305.
 PR 29-MAR-1996; US-626186.
 PA (BIOM-) BIOMEASURE INC.
 PI Dong ZX;
 DR WPI: 97-118819/11.
 PT New variants of human parathyroid hormone 1-34 peptide - which
 PT stimulate bone growth and are used for treatment of osteoporosis and
 PT bone fracture
 PS Claim 11; Page -: 33pp; English.
 CC The present sequence is a specific example of a human parathyroid
 CC hormone (hPTH) analogue from fragment 1-34 in which at least one
 CC of the amino acid residues at positions 3, 12, 16, 17, 19 and 34
 CC is alpha-aminoisobutyric acid (Aib). In this example the Ser residue
 CC at position 3 of the wild-type has been substituted by Aib. The hPTH
 CC analogues stimulate bone growth and so are useful in human or veterinary
 CC medicine for treatment of osteoporosis and bone fracture, optionally in
 CC conjunction with anti-resorptive therapy (bisphosphonates and
 CC calcitonin).
 CC N.B. The present sequence does not appear in the specification. It
 CC corresponds to the known hPTH 1-34 fragment with the modifications
 CC as stated in the claim.
 SQ Sequence 34 AA;

Query Match 100.0%; Score 62; DB 22; Length 34;
 Best Local Similarity 100.0%; Pred. No. 4.68e+00;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 hnlgkhlns 17
 QY 1 HNLGKHLNS 9

Search completed: Thu Jul 30 10:27:26 1998
 Job time : 15 secs.

COMMENT Resolution: not applicable
 COMMENT Determination: NMR
 KEYWORDS hormone
 FEATURE
 15-25
 SUMMARY

#region helix (right hand alpha)
 #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 62; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 4.02e-03;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 6 HNLGRHNS 14
 QY 1 HNLGRHNS 9

Search completed: Thu Jul 30 10:26:53 1998
 Job time : 28 secs.

W D S E L F (TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:25:15 1998; Maspar time 2.12 Seconds
106.609 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-13
Description: (1-9) from US08817547A.pep
Perfect Score: 62
Sequence: 1 HNLGKHLNS 9

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 22.158; Variance 22.443; scale 0.987

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	62	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	1.55e-04
2	58	93.5	115	1	PTHY_PIG PARATHYROID HORMONE PR	2.07e-03
3	58	93.5	115	1	PTHY_CANFA PARATHYROID HORMONE PR	2.07e-03
4	58	93.5	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	2.07e-03
5	57	91.9	115	1	PTHY_RAT PARATHYROID HORMONE PR	3.90e-03
6	48	77.4	171	1	PLA_BACSU PROTEASE SYNTHASE AND	8.66e-01
7	47	75.8	621	1	JUNCTION PLAKOGLOBIN (1.52e+00
8	47	75.8	738	1	PLAK_XENLA JUNCTION PLAKOGLOBIN (1.52e+00
9	47	75.8	743	1	PLAK_HUMAN JUNCTION PLAKOGLOBIN (1.52e+00
10	45	72.6	187	1	ATPD_ODOSI ATP SYNTHASE DELTA CHA	4.57e+00
11	45	72.6	381	1	DHB2_MOUSE ESTRADIOL 17 BETA-DEHY	4.57e+00
12	44	71.0	265	1	APAL_PIG APOLIPOPROTEIN A-1 PRE	7.80e+00
13	44	71.0	317	1	KSF1_ECOLI KPSF PROTEIN.	7.80e+00
14	44	71.0	386	1	PROTEIN C17/B23.	7.80e+00
15	44	71.0	585	1	Y187_MYCG FERROCHLATASE (EC 4.9	7.80e+00
16	43	69.4	310	1	HEMZ_BACSU FERROCHLATASE (EC 4.9	1.32e+01
17	43	69.4	985	1	NAH_YEAST PROBABLE NA(+)/H(+) AN	1.32e+01
18	43	69.4	1021	1	YPT7_CAEEL HYPOTHETICAL 11.7 KD	1.32e+01
19	42	67.7	180	1	Y088_METUA HYPOTHETICAL PROTEIN M	2.21e+01
20	42	67.7	192	1	SC72_YEAST TRANSLLOCATION PROTEIN	2.21e+01
21	42	67.7	246	1	SR1A_PHYPO SPHERULIN 1A PRECURSOR	2.21e+01
22	42	67.7	292	1	YG29_YEAST HYPOTHETICAL 34.0 KD P	2.21e+01
23	42	67.7	417	1	HS47_HUMAN 47 KD HEAT SHOCK PROTE	2.21e+01

RESULT	ID	PTHY_HUMAN	STANDARD:	PRF:	115 AA.
AC	P01270:				
DT	21-JUL-1986 (REL. 01, CREATED)				
DT	13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).				
GN	PTH.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
CC	EUTHERIA; PRIMATES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE: 82150870.				
RA	HENDY G.N., KRONENBERG H.M., POTTS J.T., JR., RICH A.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE: 83169834.				
RA	VASICER T.J., MCCREYTT B.E., FREEMAN M.W., FENNICK B.J.,				
RA	HENDY G.N., POTTS J.T., JR., RICH A., KRONENBERG H.M.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 80:2127-2131(1983).				
RN	[3]				
RP	SEQUENCE OF 26-37.				
RA	MEDLINE: 74174967.				
RA	JACOBS J.W., KEMPER B., NIALL H.D., HABENER J.F., POTTS J.T., JR.;				
RL	NATURE 249:155-157(1974).				
RN	[4]				
RP	SEQUENCE OF 32-68.				
RA	MEDLINE: 74111656.				
RA	NIALL H.D., SAUER R.T., JACOBS J.W., KEUTMANN H.T., SEGRE G.V.,				
RA	O'RIORDAN J.L.H., AUBRECH G.D., POTTS J.T., JR.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).				
RN	[5]				
RP	SEQUENCE OF 61-83 AND 84-115.				
RA	MEDLINE: 79082855.				
RA	KEUTMANN H.T., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.,				
RA	POTTS J.T., JR.;				
RL	BIOCHEMISTRY 17:5723-5729(1978).				
RN	[6]				
RP	SEQUENCE OF 75-100.				
RA	KEUTMANN H.T., NIALL H.D., JACOBS J.W., BARLING P.M., HENDY G.N.,				
RA	O'RIORDAN J.L.H., POTTS J.T., JR.;				
RL	(IN) CALCIUM-REGULATING HORMONES, TALMADGE R.V., OWEN M.,				
RA	PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM,				
RL	(1975).				
RN	[7]				

RP REVISIONS.
 RX MEDLINE; 75146516.
 RA KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL BIOCHEMISTRY 14:1842-1847(1975).
 RN [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE; 75059220.
 RA TREGGAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D.,
 RA KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL HOPE-SETLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
 RN [9]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE; 73327467.
 RA ANDREATTA R.H., HARTMANN A., JOEHL A., KAMBER B., MAIER R.,
 RA RINKEB B., RITTEL W., SIEBER P.;
 RL HELV. CHIM. ACTA 56:470-473(1973).
 RN [10]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE; 91299748.
 RA KLAUS W., DIECKMANN T., WRAY V., SCHOMBURG D., WINGENDER E., MAYER H.;
 RL BIOCHEMISTRY 30:6936-6942(1991).
 RN [11]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE; 93345518.
 RA BARON J.A., CUTHBERTSON R.M.;
 RL EUR. J. BIOCHEM. 215:315-321(1993).
 RN [12]
 RP STRUCTURE BY NMR OF 32-68.
 RX MEDLINE; 95318084.
 RA MARX U.C., AUGSTERMANN S., BAYER P., ADERHANN K., ECHART A.,
 RA STICHT H., WALTER S., SCHMID F.-X., JAENICKE R., FORSMANN W.-G.,
 RA ROESCH P.;
 RL J. BIOL. CHEM. 270:15194-15202(1995).
 RN [13]
 RP VARIANT ARG-18.
 RX MEDLINE; 91009811.
 RA ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,
 RA KRONENBERG H.M.;
 RL J. CLIN. INVEST. 86:1084-1087(1990).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
 CC HYPOPARATHYROIDISM (FTH).
 DR EMBL; J00301; G190704; -.
 DR EMBL; V00597; G37144; -.
 DR PIR; A28146; E186700; -.
 DR PIR; A01536; PTHU.
 DR PIR; A19339; A19339.
 DR PDB; 1HPH; 10-JUL-95.
 DR PDB; 12WA; 12-MAR-97.
 DR PDB; 12WB; 12-MAR-97.
 DR PDB; 12WC; 12-MAR-97.
 DR PDB; 12WD; 12-MAR-97.
 DR PDB; 12WE; 12-MAR-97.
 DR PDB; 12WF; 16-JUN-97.
 DR PDB; 12WG; 16-JUN-97.
 DR MIM; 146200; -.
 DR MIM; 168450; -.
 DR PROSITE; PS00335; PARATHYROID; 1.
 KM HORMONE; SIGNAL; DISEASE MUTATION; 3D-STRUCTURE.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT VARIANT 18 18
 FT CONFLICT 107 107 PARATHYROID HORMONE.
 FT SEQUENCE 115 AA; 12861 MW; 243E87C7 CRC32; N->D (IN REF. 5).
 Query Match 100.0%; Score 62; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 1.55e-04;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 40 HNLGKHLNS 48
 OY 1 HNLGKHLNS 9
 RESULT 2
 ID PTH_PIG STANDARD; PRT; 115 AA.
 AC P01269;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
 OS SUS SCROFA (PIG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; ARTIODACTYLA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87316938.
 RA SCHMELZER H.-J., GROSS G., WIDERA G., MAYER H.;
 RL NUCLEIC ACIDS RES. 15:6740-6740(1987).
 RN [2]
 RP SEQUENCE OF 26-115.
 RX MEDLINE; 76018954.
 RA CHU L.L.H., HUANG W.-Y., LITLEDIKE E.T., HAMILTON J.W., COHN D.V.;
 RL BIOCHEMISTRY 14:3631-3635(1975).
 RN [3]
 RP SEQUENCE OF 32-115.
 RX MEDLINE; 74253317.
 RA SAUER R.T., NIALL H.D., HOGAN M.L., KEUTMANN H.T., O'RIORDAN J.L.H.,
 RA POTTS J.T. JR.;
 RL BIOCHEMISTRY 13:1994-1999(1974).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 DR EMBL; X05722; G1839; -.
 DR PIR; A01535; PTPC.
 DR PIR; B26806; B26806.
 DR PROSITE; PS00335; PARATHYROID; 1.
 KM HORMONE; SIGNAL.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT SEQUENCE 115 AA; 12852 MW; 98B67F47 CRC32; PARATHYROID HORMONE.
 Query Match 93.5%; Score 58; DB 1; Length 115;
 Best Local Similarity 88.9%; Pred. No. 2.07e-03;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;







Search completed: Thu Jul 30 10:25:21 1998
 Job time : 6 secs.

RA QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S., KIRKNESS E.F.,
RA DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B., PETERSON S.,
RA REICH C.I., MCNEIL L.K., BADGER J.H., GLODER A., ZHOU L., OVERBEEK R.,
RA GOCAYNE J.D., WEIDMAN J.F., McDONALD L., UTERBACK T., COTTON M.D.,
RA SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M., SADOW P.W.,
RA D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., MASON T.M.,
RA OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.,
RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RA KLENK H.P., CLAYTON R.A., TOMB J., WHITE O., NELSON K.E., KETCHUM K.A.,
RA DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D., RICHARDSON D.L.,
RA KERLAVAGE A.R., GRAHAM D.E., KYRIDES N.C., FLEISCHMANN R.D.,
RA QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S., KIRKNESS E.F.,
RA DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B., PETERSON S.,
RA REICH C.I., MCNEIL L.K., BADGER J.H., GLODER A., ZHOU L., OVERBEEK R.,
RA GOCAYNE J.D., WEIDMAN J.F., McDONALD L., UTERBACK T., COTTON M.D.,
RA SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M., SADOW P.W.,
RA D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., MASON T.M.,
RA OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.,
RA SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
EMBL: AB000982; G2648811; -
NM HYPOTHETICAL PROTEIN.
SQ SEQUENCE 421 AA: 48473 MW: D1467826 CRC32:

Query Match 79.0%; Score 49; DB 9; Length 421;
Best Local Similarity 77.8%; Pred. No. 6.15e-01;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 79 NLSKHLNS 87
:|||||
QY 1 HNLGKHLNS 9

Search completed: Thu Jul 30 10:26:08 1998
Job time : 30 secs.

Job time : 16 secs.

CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 SQ Sequence 34 AA;

Query Match 100.0%; Score 58; DB 9; Length 34;
 Best Local Similarity 100.0%; Pred. No. 7.41e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 hnlgkhln 16
 |||||
 QY 1 HNLGKHLN 8

RESULT 2
 ID W17949 standard; peptide; 34 AA.
 AC W17949;

DT 29-JUL-1997 (first entry)
 Human parathyroid hormone analogue [Cha24,28,31]hPTH(1-34)NH2.
 Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
 bone fracture.

OS Homo sapiens.
 OS Synthetic.

Location/Qualifiers
 modified_site 24
 /label- OTHER

modified_site 28
 /note- "Cyclohexylalanine (Cha)"

modified_site 31
 /note- "Cha"

modified_site 31
 /label- OTHER

modified_site 34
 /note- "Cha"

modified_site 34
 /note- "In amide form"

PN W09702834-A1.
 PD 30-JAN-1997.
 PE 03-JUL-1996; U11292.
 PR 13-JUL-1995; US-001105.
 PR 06-SEP-1995; US-003305.
 PR 29-MAR-1996; US-626186.
 PA (BIOM-) BIOMEASURE INC.
 PI Dong 2X;

DR WPI; 97-118819/11.
 PT New variants of human parathyroid hormone 1-34 peptide - which
 PT stimulate bone growth and are used for treatment of osteoporosis and
 PT bone fracture
 PT Claim 7; Page -: 33pp; English.

The present sequence is a specific example of a human parathyroid
 hormone (hPTH) analogue from fragment 1-34 in which at least one
 of the amino acid residues at positions 7, 11, 23, 24, 27, 28 and 31
 is cyclohexylalanine (Cha). In this example the Trp residue at
 CC position 24 and 28, and the Val residue at position 31 of the
 CC wild-type have been substituted by Cha. The hPTH analogues stimulate
 CC bone growth and so are useful in human or veterinary medicine for
 CC treatment of osteoporosis and bone fracture, optionally in conjunction
 CC with anti-resorptive therapy (bisphosphonates and calcitonin).
 CC N.B. The present sequence does not appear in the specification. It
 CC corresponds to the known hPTH 1-34 fragment with the modifications
 CC as stated in the claim.
 SQ Sequence 34 AA;

Query Match 100.0%; Score 58; DB 22; Length 34;
 Best Local Similarity 100.0%; Pred. No. 7.41e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 hnlgkhln 16
 |||||
 QY 1 HNLGKHLN 8

Search completed: Thu Jul 30 10:29:43 1998

WIDEVIEW (TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:28:51 1998; MasPar time 3.31 Seconds
Tabular output not generated. 88.370 Million cell updates/sec

Title: >US-08-817-547A-14
Description: (1-8) from US08817547A.pep
Perfect Score: 58
Sequence: 1 HNLGKHLN 8

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr56
1:plr1 2:plr2 3:plr3 4:plr4 5:nr13d

Statistics: Mean 20.760; Variance 25.957; scale 0.800

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description	Pred. No.
1	58	100.0	34	5	12WA	parathyroid hormone (1.85e-02
2	58	100.0	34	5	12WE	parathyroid hormone (1.85e-02
3	58	100.0	34	5	12WF	parathyroid hormone (1.85e-02
4	58	100.0	34	5	12WG	parathyroid hormone (1.85e-02
5	58	100.0	35	5	12WD	parathyroid hormone (1.85e-02
6	58	100.0	35	5	12WB	parathyroid hormone (1.85e-02
7	58	100.0	37	5	12PH	parathyroid hormone (1.85e-02
8	58	100.0	37	5	12PH	parathyroid hormone (1.85e-02
9	58	100.0	34	5	12WH	cyclic parathyroid hormone (1.85e-02
10	54	93.1	37	5	12WC	parathyroid hormone (1.54e-01
11	54	93.1	115	1	PTBO	parathyroid hormone (1.54e-01
12	54	93.1	115	1	PTPG	parathyroid hormone (1.54e-01
13	54	93.1	115	2	UC4202	parathyroid hormone (1.54e-01
14	53	91.4	105	2	151851	parathyroid hormone - 2.59e-01
15	53	91.4	115	2	A05091	parathyroid hormone - 2.59e-01
16	48	82.8	172	2	A35145	transcriptional regul 3.18e+00
17	48	82.8	172	2	E69671	hypothetical protein 1.33e+01
18	45	77.6	421	2	E69467	hypothetical protein 2.12e+01
19	44	75.9	231	2	U00704	apolipoprotein A-I - 2.12e+01
20	44	75.9	264	2	S31394	apolipoprotein A-I - 2.12e+01
21	44	75.9	264	2	A46018	apolipoprotein A-I - 2.12e+01
22	44	75.9	386	2	D42528	B23R protein - vaccin 2.12e+01
23	44	75.9	568	2	S76244	hypothetical protein 2.12e+01

24	44	75.9	585	2	G64220	ATP-binding protein m 2.12e+01
25	43	74.1	308	5	1AK1	ferrochelatase (EC 4. 3.35e+01
26	43	74.1	310	5	1FJ1	ferrochelatase (EC 4. 3.35e+01
27	43	74.1	310	2	C47045	ferrochelatase (EC 4. 3.35e+01
28	43	74.1	619	2	S54636	probable membrane pro 3.35e+01
29	43	74.1	621	2	S35092	plakoglobin - mouse (3.35e+01
30	43	74.1	738	2	S35093	plakoglobin - African 3.35e+01
31	43	74.1	744	2	A432905	plakoglobin, desmosom 3.35e+01
32	43	74.1	1021	2	S44644	F37A4.7 protein - Cae 3.35e+01
33	42	72.4	180	2	H64310	hypothetical protein 5.26e+01
34	42	72.4	243	2	B29624	spherulin 1b precurs 5.26e+01
35	42	72.4	292	2	S64361	hypothetical protein 5.26e+01
36	42	72.4	480	2	F69505	thymidylate synthase 5.26e+01
37	42	72.4	1447	2	S63669	ubiquitin--protein 11 5.26e+01
38	42	72.4	1950	2	S12332	polyketide synthase p 5.26e+01
39	42	72.4	4930	2	E69679	heat shock protein Hs 8.18e+01
40	41	70.7	417	1	S20608	heat shock protein Hs 8.18e+01
41	41	70.7	417	1	A40968	probable RNA-directed 8.18e+01
42	41	70.7	513	2	S21976	hypothetical protein 8.18e+01
43	41	70.7	592	2	D64044	cyclic peptide synthe 8.18e+01
44	41	70.7	1401	2	S77657	RNA-directed RNA poly 8.18e+01
45	41	70.7	1444	1	A43377	

ALIGNMENTS

RESULT	1	12WA	#type complete
ENTRY		parathyroid hormone (residues 1-34) - human	
TITLE		HPTH(1-34)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 1-34, NMR 10	
PDB_TITLE		structures	
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67856	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WA	
REFERENCE		TN001717	
#authors		Marx, U.C.	
#book		In Strukturen Verschiedener Parathormonfragmente In Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996	
COMMENT		Resolution: not applicable	
KEYWORDS		Determination: NMR	
FEATURE		hormone	
6-9		#region helix (right hand alpha)\	
19-30		#region helix (right hand alpha)	
SUMMARY		#length 34 #molecular-weight 4118 #checksum 5629	
Query Match		100.0%; Score 58; DB 5; Length 34;	
Best Local Similarity		100.0%; Pred. No. 1.85e-02;	
Matches		8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	9	HNLGKHLN 16	
Qy	1	HNLGKHLN 8	
RESULT	2	12WE	#type complete
ENTRY		parathyroid hormone (residues 4-37) - human	
TITLE		HPTH(4-37)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 4-37, NMR 10	
PDB_TITLE		structures	
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67860	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WE	
REFERENCE		TN001721	
#authors		Marx, U.C.	
#book		In Strukturen Verschiedener Parathormonfragmente In Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996	

COMMENT Resolution: not applicable
 COMMENT Determination: NMR
 KEYWORDS hormone
 FEATURE
 15-25
 SUMMARY

#region helix (right hand alpha)
 #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 58; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.85e-02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 HNLGKHLN 13
 QY 1 HNLGKHLN 8

Search completed: Thu Jul 30 10:29:09 1998
 Job time : 18 secs.

RP REVISIONS.
 RX MEDLINE: 75146516.
 RA KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL BIOCHEMISTRY 14:1842-1847(1975).
 (8)
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 75059220.
 RA TREGGAR G.W., VAN RIENSCHOTEN J., GREEN E., NIALL H.D.,
 RA KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
 (9)
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 73327467.
 RA ANDREATTA R.H., HARTMANN A., JOEHL A., KAMBER B., MAIER R.,
 RA REINER B., RITTEL W., SIEBER P.;
 RL HELV. CHIM. ACTA 56:470-473(1973).
 (10)
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE: 91299748.
 RA KLAUS W., DIECKMANN T., WRAY V., SCHOMBURG D., WINGENDER E., MAYER H.;
 RL BIOCHEMISTRY 30:6936-6942(1991).
 (11)
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE: 93345518.
 RA BARDEN J.A., CUTHERSON R.M.;
 RL EUR. J. BIOCHEM. 215:315-321(1993).
 (12)
 RP STRUCTURE BY NMR OF 32-68.
 RX MEDLINE: 95318084.
 RA MARK U.C., AUSTERMANN S., BAYER P., ADERMAN K., ECHART A.,
 RA STICHT H., WALTER S., SCHMID F.-X., JAENICKE R., FORSSMANN W.-G.,
 RA ROESCH P.;
 RL J. BIOL. CHEM. 270:15194-15202(1995).
 (13)
 RP VARIANT ARG-18.
 RX MEDLINE: 91009811.
 RA ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,
 RA KRONENBERG H.M.;
 RL J. CLIN. INVEST. 86:1084-1087(1990).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
 HYPOPARATHYROIDISM (FTH).
 CC EMBL: J00301; G190704; -.
 DR EMBL: V00597; G37144; -.
 DR EMBL: A29146; E186700; -.
 DR PIR: A01536; PTHU.
 DR PIR: A15339; A19339.
 DR PDB: 1HPH; 10-JUL-95.
 DR PDB: 1HTH; 15-OCT-97.
 DR PDB: 1ZWA; 12-MAR-97.
 DR PDB: 1ZMB; 12-MAR-97.
 DR PDB: 1ZMC; 12-MAR-97.
 DR PDB: 1ZMD; 12-MAR-97.
 DR PDB: 1ZME; 12-MAR-97.
 DR PDB: 1ZWF; 16-JUN-97.
 DR PDB: 1ZWG; 16-JUN-97.
 DR MIM: 146200; -.
 DR MIM: 168450; -.
 DR PROSITE: PS00335; PARATHYROID; 1.
 KW HORMONE; SIGNAL; DISEASE MUTATION; 3D-STRUCTURE.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT VARIANT 18 18
 FT CONFLICT 107 107
 FT SEQUENCE 115 AA; 12861 MW; 243887C7 CRC32;
 SQ

Query Match 100.0%; Score 58; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 8.80e-04;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 40 HNKGKHLN 47
 OY 1 HNKGKHLN 8
 RESULT 2
 ID PTHY_PIG STANDARD; PRT; 115 AA.
 AC P01269;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
 GN PTH.
 OS SUS SCROFA (PTG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; ARTIODACTYLA.
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 87316938.
 RA SCHWEIZER H.-J., GROSS G., WIDERA G., MAYER H.;
 RL NUCLEIC ACIDS RES. 15:6740-6740(1987).
 RN (2)
 RP SEQUENCE OF 26-115.
 RX MEDLINE: 76018954.
 RA CHU L.L.H., HUANG W.-Y., LITLEDIKE E.T., HAMILTON J.W., COHN D.V.;
 RL BIOCHEMISTRY 14:3631-3635(1975).
 RN (3)
 RP SEQUENCE OF 32-115.
 RX MEDLINE: 74253317.
 RA SAUER R.T., NIALL H.D., HOGAN M.L., KEUTMANN H.T., O'RIORDAN J.L.H.,
 RA POTTS J.T. JR.;
 RL BIOCHEMISTRY 13:1994-1999(1974).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC EMBL: X05722; G1839; -.
 DR PIR: A01535; PTPG.
 DR PIR: B26806; B26806.
 DR PROSITE: PS00335; PARATHYROID; 1.
 KW HORMONE; SIGNAL.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT SEQUENCE 115 AA; 12852 MW; 98B67F47 CRC32;
 SQ

Query Match 93.1%; Score 54; DB 1; Length 115;
 Best Local Similarity 87.5%; Pred. No. 1.17e-02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Search completed: Thu Jul 30 10:27:51 1998
 Job time : 6 secs.

RA BORISS R., BOHRSTER L., BRANS A., BRAUN M., BRIGNEL S.C., BRON S.,
RA BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
RA CHOI S.K., CODANI J.J., CONNERTON I.F., COWINGS N.J., DANIEL R.A.,
RA DENIZOT F., DEVINE K.M., DUSTERHOFF A., EHRLICH S.D., EMERSON P.A.,
RA ENTIAN K.D., ERLINGTON J., FABER C., FERRARI E., FOULGER D., FRITZ C.,
RA FUJITA M., FUJITA Y., FUMA S., GALIZZI A., GALLERON N., GHIM S.Y.,
RA GLASER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G., GUISEPI G., GUY B.J.,
RA HAGA K., HAIECH J., HARWOOD C.R., HENAUT A., HILBERT H., HOLSAPPEL S.,
RA HOSONO S., HULLO M.F., IITAYA M., JONES L., JORIS B., KARAMAYA D.,
RA KASHIHARA Y., KLAERR-BLANCHARD M., KLEIN C., KOBAYASHI Y., KOETTER P.,
RA KONINGSTEIN G., KROGH S., KUMANO M., KURITA K., LAPIDUS A.,
RA LARDINOIS S., LAUBER J., LAZAREVIC V., LEE S.M., LEVINE A., LIU H.,
RA MASUDA S., MAUEL C., MEDIGUE C., MEDINA N., MELLAO R.P., MIZUNO M.,
RA MOESTL D., NAKAI S., NOBACK M., NOONE D., O'REILLY M., OGAMA K.,
RA OGIMAWA A., ODEGA B., PARK S.H., PARO V., POHL T.M., PORTETELLE D.,
RA RAPOPORT G., PRESCOTT A.M., PRESCAN E., PUJIC P., PURNELLE B.,
RA ROCHE B., ROSE M., REYNOLDS S., RIEGER M., RIVOLTA C., ROCHA E.,
RA SCHROETER R., SCOFFONE F., SEKIGUCHI J., SEKONSKA A., SEROR S.J.,
RA SERRO P., SHIN B.S., SOLO B., SOROKIN A., TACCONE E., TAKAGI T.,
RA TAKAHASHI H., TAKEMARU K., TAKEUCHI M., TAMAKOSHI A., TANAKA T.,
RA TERPSTRA P., TOGNONI A., TOSATO V., UCHIYAMA S., YANDENBOL M.,
RA VANIER F., VASSAROTTI A., VIARI A., WAMUTT R., WEDLER E., WEDLER H.,
RA YASUMOTO K., YATA K., WINTERS P., WIPAT A., YAMAMOTO H., YAMANE K.,
RA YOSHIKAWA H., YAMCHIN A., YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E.,
RL NATURE 390:249-256(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-168;
RA KUNST F., OGASAWARA N., YOSHIKAWA H., YAMCHIN A.,
RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: 299120; E184294.
SQ SEQUENCE 172 AA; 20015 MW; 2AA7F8CE CRC32;

Query Match 82.8%; Score 48; DB 9; Length 172;
Best Local Similarity 85.7%; Pred. No. 5.95e-01;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 105 HGLGKHL 111
QY 1 HNLGKHL 7

Search Completed: Thu Jul 30 10:28:33 1998
Job time : 25 secs.

Db 3 hnlgkhl 9
 |||||
 QY 1 HNLGKHL 7

RESULT

ID R62432 standard; peptide: 34 AA.
 AC R62432;
 DT 31-JUL-1995 (first entry)
 DE Accelerator peptide basic region peptide, P-8
 KW Accelerator; basic amino acid; cell growth factor; gingiva;
 KM periodontal tissue; regeneration; periodontitis; periodontal pocket;
 OS down growth; epithelium; fibre adhesion; cement.
 PN J06234653-A.
 PD 23-AUG-1994.
 PF 10-FEB-1993; JP-045998.
 PR (SUNZ) SUNSTAR CHEM IND CO LTD.
 WP1: 95-157631/21.
 Accelerator for regenerating periodontal tissue - comprises
 peptide having 3-34 aminoacid residues having connected basic
 aminoacid residues
 PT aminoacid residues
 PS Disclosure: Page 3: 7pp; Japanese.
 CC The sequences in R62425-36 are peptide fragments of an accelerator
 protein which contain at least two basic amino acids. The accelerator
 also comprises a cell growth factor. The accelerator may be used to
 accelerate the growth of periodontal tissue regeneration. The
 accelerator is applied by opening the gingiva, treating the tissue
 destroyed by periodontitis and applying the accelerator in the
 periodontal pocket. The accelerator reduces the down growth of the
 epithelium and accelerates fibre adhesion and regenerates cement.
 SQ Sequence 34 AA;

Query Match 100.0%; Score 53; DB 26; Length 34;
 Best Local Similarity 100.0%; Pred. No. 9.01e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 9 hnlgkhl 15
 |||||
 QY 1 HNLGKHL 7

Search completed: Thu Jul 30 10:31:31 1998
 Job time : 16 secs.

 WIRE (TM)

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msrch_pp protein - protein database search, using Smith-Waterman algorithm
 on: Thu Jul 30 10:30:52 1998; Maspar time 4.09 Seconds
 Tabular output not generated. 62.524 Million cell updates/sec

Title: >US-08-817-547A-15
 Description: (1-7) from US08817547A.pep
 Perfect Score: 53
 Sequence: 1 HNLGKHL 7

Scoring table: PAM 150
 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: plr56
 1:plr1 2:plr2 3:plr3 4:plr4 5:nrl3d

Statistics: Mean 20.217; Variance 24.497; scale 0.825

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	53	100.0	34	5	12WG parathyroid hormone 4	1.17e-01
2	53	100.0	34	5	12WF parathyroid hormone 4	1.17e-01
3	53	100.0	34	5	12WE parathyroid hormone (1.17e-01
4	53	100.0	34	5	12WA parathyroid hormone (1.17e-01
5	53	100.0	35	5	12WD parathyroid hormone (1.17e-01
6	53	100.0	36	5	12WB parathyroid hormone (1.17e-01
7	53	100.0	37	5	12WH parathyroid hormone (1.17e-01
8	53	100.0	37	5	12WC parathyroid hormone (1.17e-01
9	53	100.0	105	2	151851 parathyroid hormone -	1.17e-01
10	53	100.0	115	2	UC4202 parathyroid hormone -	1.17e-01
11	53	100.0	115	2	A05091 parathyroid hormone p	1.17e-01
12	53	100.0	115	1	PTHU parathyroid hormone p	1.17e-01
13	53	100.0	115	1	PTBO parathyroid hormone p	1.17e-01
14	53	100.0	115	1	PRPG parathyroid hormone p	1.17e-01
15	50	94.3	34	5	1HTH cyclic parathyroid ho	1.62e+00
16	48	90.6	172	2	A35145 transcriptional regul	1.62e+00
17	48	90.6	172	2	E68671 transcriptional regul	1.62e+00
18	44	83.0	585	2	G64220 ATP-binding protein m	1.18e+01
19	43	81.1	621	2	S35092 plakoglobin - mouse	1.91e+01
20	43	81.1	738	2	S35093 plakoglobin - African	1.91e+01
21	43	81.1	744	2	A32905 plakoglobin, desmosom	1.91e+01
22	43	81.1	1021	2	S44644 F37A4.7 protein - Cae	1.91e+01
23	42	79.2	243	2	B29624 spherulin 1b precuro	3.07e+01

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
24	42	79.2	480	2	E69505 thymidylate synthase	3.07e+01
25	42	79.2	619	2	S54636 probable membrane pro	3.07e+01
26	41	77.4	246	2	S01789 pyruvate formate-lyas	4.89e+01
27	41	77.4	386	2	D45228 B23R protein - vaccin	4.89e+01
28	41	77.4	405	1	A41252 heat shock protein 47	4.89e+01
29	41	77.4	417	1	A42843 heat shock protein Hs	4.89e+01
30	41	77.4	417	1	A40968 heat shock protein 47	4.89e+01
31	41	77.4	417	1	S20608 heat shock protein Hs	4.89e+01
32	41	77.4	418	1	I52968 collagen-2 - human	4.89e+01
33	41	77.4	568	2	S76244 hypotetical protein	4.89e+01
34	41	77.4	4930	2	E69679 polyketide synthase p	4.89e+01
35	40	75.5	160	2	S80066 probable olfactory re	7.71e+01
36	40	75.5	180	2	H84310 hypotetical protein	7.71e+01
37	40	75.5	209	2	D51119 protocatechuate 3,4-d	7.71e+01
38	40	75.5	291	2	S73826 MG240 homolog F10-orf	7.71e+01
39	40	75.5	292	2	E64226 hypotetical protein	7.71e+01
40	40	75.5	421	2	E69467 hypotetical protein	7.71e+01
41	40	75.5	513	2	S21976 probable RNA-directed	7.71e+01
42	40	75.5	773	2	A46627 carnitine palmitoylitr	7.71e+01
43	40	75.5	1401	2	S77657 cyclic peptide synthe	7.71e+01
44	40	75.5	1444	1	A43377 RNA-directed RNA poly	7.71e+01
45	40	75.5	1447	2	S63669 UDPglucose--glycoprot	7.71e+01

ALIGNMENTS

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	53	100.0	34	5	12WG parathyroid hormone 4	1.17e-01
2	53	100.0	34	5	12WF parathyroid hormone 4	1.17e-01
3	53	100.0	34	5	12WE parathyroid hormone (1.17e-01
4	53	100.0	34	5	12WA parathyroid hormone (1.17e-01
5	53	100.0	35	5	12WD parathyroid hormone (1.17e-01
6	53	100.0	36	5	12WB parathyroid hormone (1.17e-01
7	53	100.0	37	5	12WH parathyroid hormone (1.17e-01
8	53	100.0	37	5	12WC parathyroid hormone (1.17e-01
9	53	100.0	105	2	151851 parathyroid hormone -	1.17e-01
10	53	100.0	115	2	UC4202 parathyroid hormone -	1.17e-01
11	53	100.0	115	2	A05091 parathyroid hormone p	1.17e-01
12	53	100.0	115	1	PTHU parathyroid hormone p	1.17e-01
13	53	100.0	115	1	PTBO parathyroid hormone p	1.17e-01
14	53	100.0	115	1	PRPG parathyroid hormone p	1.17e-01
15	50	94.3	34	5	1HTH cyclic parathyroid ho	1.62e+00
16	48	90.6	172	2	A35145 transcriptional regul	1.62e+00
17	48	90.6	172	2	E68671 transcriptional regul	1.62e+00
18	44	83.0	585	2	G64220 ATP-binding protein m	1.18e+01
19	43	81.1	621	2	S35092 plakoglobin - mouse	1.91e+01
20	43	81.1	738	2	S35093 plakoglobin - African	1.91e+01
21	43	81.1	744	2	A32905 plakoglobin, desmosom	1.91e+01
22	43	81.1	1021	2	S44644 F37A4.7 protein - Cae	1.91e+01
23	42	79.2	243	2	B29624 spherulin 1b precuro	3.07e+01

Thu Jul 30 13:37:57 1998

US-08-817-547A-15.rpt

Page 2

pp.0, Bayreuth : University of Bayreuth (Thesis), 1996
COMMENT Resolution: not applicable
COMMENT Determination: NMR
KEYWORDS disease mutation; hormone; signal
FEATURE
3-6 #region helix (right hand alpha)\
14-27 #region helix (right hand alpha)
SUMMARY #length 34 #molecular-weight 4128 #checksum 5508
Query Match 100.0%; Score 53; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.17e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 6 HNLGKHL 12
QY 1 HNLGKHL 7

Search completed: Thu Jul 30 10:30:57 1998
Job time : 5 secs.

M05050161

(TM)

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March, 1998 protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:30:01 1998; Maspar time 2.13 Seconds
Tabular output not generated. 82.367 Million cell updates/sec

Title: >US-08-817-547A-15
(1-7) from US08817547A.pep
Description: 53
Perfect Score: 53
Sequence: 1 HNLGKHL 7

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prots5
1:swlslsl

Statistics: Mean 21.123; Variance 20.163; scale 1.048

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	53	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	8.04e-03
2	53	100.0	115	1	PTHY_BOVINA PARATHYROID HORMONE PR	8.04e-03
3	53	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	8.04e-03
4	53	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	8.04e-03
5	53	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	8.04e-03
6	48	90.6	171	1	PARA_BACCU PARATHYROID HORMONE PR	1.98e-01
7	44	83.0	585	1	Y187_MYCGE HYPOTHETICAL ABC TRANS	2.21e+00
8	43	81.1	621	1	PLAK_MOUSE JUNCTION PLAKGLOBIN (3.95e+00
9	43	81.1	738	1	PLAK_XENLA JUNCTION PLAKGLOBIN (3.95e+00
10	43	81.1	743	1	YPT7_CAEBL JUNCTION PLAKGLOBIN (3.95e+00
11	43	81.1	1021	1	SPHRULIN 1A PRECURSOR	6.98e+00
12	42	79.2	246	1	SRIA_PHYPO ESTRADIOL 17 BETA-DEHY	6.98e+00
13	42	79.2	381	1	DHB2_MOUSE PROBABLE RIBOSOMAL PRO	1.22e+01
14	41	77.4	105	1	YBAF_STAUA PYRUVATE FORMATE-LYASE	1.22e+01
15	41	77.4	245	1	PELA_ECOLI PROTEIN C17/B23.	1.22e+01
16	41	77.4	386	1	VC17_VACCC PROTEIN C17/B23.	1.22e+01
17	41	77.4	405	1	HS47_CHICK 47 KD HEAT SHOCK PROTE	1.22e+01
18	41	77.4	417	1	HS47_RAT 47 KD HEAT SHOCK PROTE	1.22e+01
19	41	77.4	417	1	HS47_MOUSE 47 KD HEAT SHOCK PROTE	1.22e+01
20	41	77.4	417	1	HS47_HUMAN 47 KD HEAT SHOCK PROTE	1.22e+01
21	41	77.4	418	1	CBP2_HUMAN COLLAGEN-BINDING PROTE	1.22e+01
22	40	75.5	40	1	CPH1_MOUSE MITOCHONDRIAL CARINITIN	2.11e+01
23	40	75.5	96	1	VPR_HVINS VPR PROTEIN (R ORF PRO	2.11e+01

Result ID	1	PTHY_BOVIN	STANDARD;	PTHY;	115 AA.
AC	P01268;				
DT	21-JUL-1986 (REL. 01, CREATED)				
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).				
GN	PTH.				
OS	BOS TAURUS (BOVINE).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	ETHERIA; ARTIODACTYLA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 80056617.				
RA	KRONENBERG H.M., MCDEVITT B.E., MAJZUB J.A., NATHANS J., SHARP P.A.,				
RL	POTTS J.T., JR., RICH A.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 82037785.				
RA	WEAVER C.A., GORDON D.F., KEMPER B.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 84262483.				
RA	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;				
RL	GENE 28:319-329(1984).				
RN	[5]				
RP	SEQUENCE OF 26-115.				
RX	MEDLINE; 74142666.				
RA	HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,				
RL	COIN D.V.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).				
RN	[6]				
RP	SEQUENCE OF 32-115.				
RX	MEDLINE; 71076162.				
RA	NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAMSON B.F.,				
RL	AUBACH G.D., POTTS J.T. JR.;				
RL	HOPPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).				
RN	[7]				
RP	SEQUENCE OF 32-115.				
RX	MEDLINE; 71063634.				

Result ID	1	PTHY_BOVIN	STANDARD;	PTHY;	115 AA.
24	40	75.5	180	1	Y088_METIA HYPOTHETICAL PROTEIN M
25	40	75.5	209	1	PCXA_ACTIA PROTOCATECHUATE 3,4-DI
26	40	75.5	291	1	Y240_MYCPN HYPOTHETICAL PROTEIN M
27	40	75.5	292	1	Y240_MYCGE HYPOTHETICAL PROTEIN M
28	40	75.5	586	1	Y187_MYCPN HYPOTHETICAL ABC TRANS
29	40	75.5	614	1	Y022_CAEBL HYPOTHETICAL 69.0 KD P
30	40	75.5	773	1	CPH1_RAT MITOCHONDRIAL CARINITIN
31	40	75.5	1444	1	RRPL_RDV RNA-DIRECTED RNA POLYM
32	39	73.6	135	1	Y315_METIA HYPOTHETICAL PROTEIN M
33	39	73.6	171	1	YB11_HAEIN HYPOTHETICAL PROTEIN H
34	39	73.6	192	1	Y0HD_ECOLI HYPOTHETICAL 21.4 KD P
35	39	73.6	215	1	VIF_HV2DI VISION INEFFECTIVITY FAC
36	39	73.6	261	1	Y07H_MYCTU HYPOTHETICAL TRANSCRIP
37	39	73.6	292	1	Y629_YEAST HYPOTHETICAL 34.0 KD P
38	39	73.6	330	1	RCBM_EYRSP REACTION CENTER PROTEI
39	39	73.6	362	1	AROB_BACCU 3-DEHYDROQUINATE SYNTH
40	39	73.6	416	1	CCA_HAEIN TRNA NUCLEOTIDYLTRANSF
41	39	73.6	480	1	DISA_TRIGA PURINATIVE VENOM METALLO
42	39	73.6	781	1	YSPH_CAEBL HYPOTHETICAL 91.0 KD P
43	39	73.6	1713	1	LMA3_HUMAN LAMININ ALPHA-3 CHAIN
44	39	73.6	1886	1	GP21_RAT INTEGRAL MEMBRANE GLYC
45	39	73.6	2224	1	FA5_HUMAN COAGULATION FACTOR V P

Search completed: Thu Jul 30 10:30:06 1998
 Job time : 5 secs.

RA BREWER H.B. JR., ROMAN R.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
 RN [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 71091588.
 RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NITALL H.D., SAUER R.,
 RA DEFLOS L.J., DAMSON B.F., HOGAN M.L., AUBRACH G.D.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 DR EMBL: V00106; G85; -.
 DR EMBL: J00023; G163641; -.
 DR EMBL: J00024; G163643; -.
 DR EMBL: J00024; E18249; ALT_SEQ.
 DR EMBL: J00024; E18250; ALT_INIT.
 DR EMBL: K01938; G163647; -.
 DR EMBL: M25082; G163645; -.
 DR PIR: A01334; PTBO.
 DR PIR: A24949; A24949.
 DR PROSITE: PS00335; PARATHYROID; 1.
 DR HORMONE; SIGNAL.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115 PARATHYROID HORMONE.
 FT CONFLICT 106 106 V -> G (IN REF. 4).
 SQ SEQUENCE 115 AA; 12980 MW; 673EA5F2 CRC32;

Query Match 100.0%; Score 53; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 8.04e-03;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 40 HNLGKHL 46
 QY 1 HNLGKHL 7

RESULT 2
 ID PTHX_CANFA STANDARD; PRT; 115 AA.
 AC P52212;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
 GN PTH.
 OS CANIS FAMILIARIS (DOG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUThERIA; CARNIVORA.
 RN [1]
 RN SEQUENCE FROM N.A.
 RN TISSUE-PARATHYROID.
 RN MEDLINE: 95369696.
 RA ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,
 RA DERMILLE J.W., CAPEN C.C.;
 RL GENE 160:241-243(1995).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 DR EMBL: U15662; G558916; -.
 DR PROSITE: PS00335; PARATHYROID; 1.
 KW HORMONE; SIGNAL.
 FT SIGNAL 1 25 BY SIMILARITY.
 FT PROPEP 26 31 BY SIMILARITY.
 FT CHAIN 32 115 PARATHYROID HORMONE.
 SQ SEQUENCE 115 AA; 12957 MW; 16ED0EBC CRC32;

Query Match 100.0%; Score 53; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 8.04e-03;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 40 HNLGKHL 46
 QY 1 HNLGKHL 7

NWHEE

(TW)

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Search: protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:30:24 1998; MasPar time 3.61 Seconds
Tabular output not generated. 81.661 Million cell updates/sec

Title: >US-08-817-547A-15
Description: (1-7) from US08817547A.pep
Perfect Score: 53
Sequence: 1 HNLGKHL 7

Scoring table: PAM 150
Gap 15

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_protein 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 20.260; Variance 20.374; scale 0.994

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description	Pred. No.
1	53	100.0	105	10	PARATHYROID HORMONE (F	1.38e-02
2	48	90.6	172	9	TRANSCRIPTIONAL REGULA	3.17e-01
3	44	83.0	96	11	VPR PROTEIN.	3.38e+00
4	43	81.1	171	2	PIAOGLOBIN (FRAGMENT)	5.98e+00
5	43	81.1	312	3	COSMID T07E3.	5.98e+00
6	43	81.1	745	2	PIAOGLOBIN.	5.98e+00
7	43	81.1	745	10	PIAOGLOBIN.	5.98e+00
8	43	81.1	2272	2	KIAA0302 (FRAGMENT).	5.98e+00
9	42	79.2	96	11	VPR PROTEIN.	1.05e+01
10	42	79.2	123	2	WNT-LIKE PROTEIN WNT14	1.05e+01
11	42	79.2	381	10	17-BETA HYDROXYSTEROID	1.05e+01
12	42	79.2	480	9	THYMIDYLATE SYNTHASE.	1.05e+01
13	42	79.2	619	1	CHROMOSOME XV READING	1.05e+01
14	42	79.2	979	8	HYPOTHETICAL 110.0 KD	1.05e+01
15	41	77.4	283	7	HYPOTHETICAL 31.3 KD P	1.82e+01
16	41	77.4	404	12	47 KDA HEAT SHOCK PROT	1.82e+01
17	41	77.4	568	9	HYPOTHETICAL 62.3 KD P	1.82e+01
18	41	77.4	4930	9	POLYKETIDE SYNTHASE OF	1.82e+01
19	40	75.5	41	4	CARANTHINE PALMITOYLTR	3.12e+01
20	40	75.5	95	11	ENVELOPE GLYCOPROTEIN	3.12e+01

21	40	75.5	96	11	Q79793	ISOLATE N15, COMPLETE	3.12e+01
22	40	75.5	96	11	Q79233	VPR PROTEIN.	3.12e+01
23	40	75.5	96	11	Q79249	VPR PROTEIN.	3.12e+01
24	40	75.5	160	10	Q62336	OLFACTORY RECEPTOR 33	3.12e+01
25	40	75.5	367	10	Q63778	HYPOTHETICAL 43.7 KD P	3.12e+01
26	40	75.5	421	9	Q28532	HYPOTHETICAL 48.5 KD P	3.12e+01
27	40	75.5	440	9	P77814	PROLIDASE (EC 3.4.13.9	3.12e+01
28	40	75.5	513	10	Q53289	L1 RETROPOSON, ORF2 MR	3.12e+01
29	40	75.5	563	9	Q48722	RELAXASE.	3.12e+01
30	40	75.5	576	2	Q41447	KIAA134 PROTEIN (KIAA	3.12e+01
31	40	75.5	584	9	Q48665	MOBILIZATION PROTEIN.	3.12e+01
32	40	75.5	643	10	Q35948	HOMOLOG OF HUMAN WEENE	3.12e+01
33	40	75.5	764	10	Q35288	CARITINE PALMITOYLTRA	3.12e+01
34	40	75.5	831	1	Q13705	HYPOTHETICAL 95.0 KD P	3.12e+01
35	40	75.5	833	1	Q13620	HYPOTHETICAL 93.7 KD P	3.12e+01
36	40	75.5	1300	10	P97692	L1 RETROPOSON ORF	3.12e+01
37	40	75.5	1401	10	Q09053	WERNER SYNDROME.	3.12e+01
38	40	75.5	1401	9	Q50177	PROBABLE CYCLIC SYNTH	3.12e+01
39	40	75.5	1444	11	Q38631	RNA-DEPENDENT RNA POLY	3.12e+01
40	40	75.5	1447	1	Q09140	UDP-GLC:GLYCOPROTEIN G	3.12e+01
41	40	75.5	1817	3	Q19931	COSMID F31D5.	5.31e+01
42	39	73.6	191	10	Q61633	EN-2/LACZ FUSION PROTE	5.31e+01
43	39	73.6	453	11	Q83077	BETA-B PROTEIN.	5.31e+01
44	39	73.6	480	12	Q90220	PREPRO-HAIXSTATIN PREC	5.31e+01
45	39	73.6	534	9	Q60171	MODIFICATION METHYLASE	5.31e+01

ALIGNMENTS

RESULT	ID	1	PRELIMINARY:	PRT:	105 AA.
AC	Q63473				
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)				
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)				
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE (FRAGMENT).				
GN	PTH.				
OS	RATTUS NORVEGICUS (RAT).				
OC	EUROTA; METAFOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
CC	EUROTA; RODENTIA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-THYROID, AND PARATHYROID;				
RA	SCHMELZER H.J., GROSS G., MAYER H.;				
DR	ADV. GENE TECHNOL. 21:228-229(1984).				
FT	EMBL; M54875; G601933; -				
FT	NON TER 1				
SQ	SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;				
Query Match 100.0%; Score 53; DB 10; Length 105;					
Best Local Similarity 100.0%; Pred. No. 1.38e-02;					
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
DB	30	HNLGKHL 36			
QY	1	HNLGKHL 7			
RESULT 2					
ID	Q32112	PRELIMINARY:	PRT:	172 AA.	
AC	Q32112				
DT	01-JAN-1998 (TREMBLREL. 05, CREATED)				
DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)				
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)				
DE	TRANSCRIPTIONAL REGULATOR.				
GN	PATA.				
OS	BACILLUS SUBTILIS.				
CC	PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-168;				
RA	KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,				
RA	AZEVEDO V., BERIERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,				

[W][I][T][E][S][P][E][E][D] (TM)

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Search: protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:33:38 1998; Maspar time 2.52 Seconds
36.475 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-16
Description: (1-6) from US08817547A.pep
Perfect Score: 45
Sequence: 1 HNLGRK 6

Scoring table: PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 13.446; Variance 33.754; scale 0.398

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description	Pred. No.
1	45	100.0	9 18	R91656	Human parathyroid hor	1.82e+01
2	45	100.0	32 18	R88840	Human parathyroid hor	1.82e+01
3	45	100.0	34 26	R62432	Accelerator peptide b	1.82e+01
4	45	100.0	34 7	R34337	Bovine parathyroid ho	1.82e+01
5	45	100.0	34 7	R34339	Bovine parathyroid ho	1.82e+01
6	45	100.0	34 18	R88834	Human parathyroid hor	1.82e+01
7	45	100.0	34 3	P82177	Sequence of parathyro	1.82e+01
8	45	100.0	34 2	R07918	Bovine parathyroid ho	1.82e+01
9	45	100.0	34 4	R22291	Human parathyroid hor	1.82e+01
10	45	100.0	34 4	R22293	Human parathyroid hor	1.82e+01
11	45	100.0	34 14	R74521	Human parathyroid hor	1.82e+01
12	45	100.0	34 7	R34366	Human parathyroid hor	1.82e+01
13	45	100.0	34 9	R58034	Isopropyl-IL8/K(scop	1.82e+01
14	45	100.0	34 22	W17958	Human parathyroid hor	1.82e+01
15	45	100.0	34 22	W17953	Human parathyroid hor	1.82e+01
16	45	100.0	34 22	W17957	Human parathyroid hor	1.82e+01
17	45	100.0	35 14	R74527	Human parathyroid hor	1.82e+01
18	45	100.0	36 9	R58242	[Lys(isopropyl)]13]-NP	1.82e+01
19	45	100.0	36 9	R58246	Acetyl-hPTH(1-36)-NH2	1.82e+01

20	45	100.0	36 9	R58257	[Propargylglycyl]-hP	1.82e+01
21	45	100.0	36 9	R58258	[D-Asp30]-hPTH(1-36)-	1.82e+01
22	45	100.0	38 9	P20248	Parathyroid hormone 1	1.82e+01
23	45	100.0	38 9	R58283	[Trp(Pmc)23]-hPTH(1-3	1.82e+01
24	45	100.0	38 9	R58036	[Gln16]-hPTH(1-38)-OH	1.82e+01
25	45	100.0	44 26	P30015	Human parathyroid hor	1.82e+01
26	45	100.0	84 27	W25687	Human parathyroid hor	1.82e+01
27	45	100.0	84 4	R23357	Bovine parathyroid ho	1.82e+01
28	45	100.0	84 4	R23266	Bovine parathyroid ho	1.82e+01
29	45	100.0	84 4	R23449	Porcine parathyroid h	1.82e+01
30	45	100.0	84 4	R33287	Bovine parathyroid ho	1.82e+01
31	45	100.0	84 5	R29554	Oxidation resistant [1.82e+01
32	45	100.0	84 5	R29567	Oxidation resistant [1.82e+01
33	45	100.0	84 4	R21154	Human parathyroid hor	1.82e+01
34	45	100.0	84 4	R23291	Porcine parathyroid h	1.82e+01
35	45	100.0	84 4	R23285	Bovine parathyroid ho	1.82e+01
36	45	100.0	84 4	R23393	Porcine parathyroid h	1.82e+01
37	45	100.0	84 4	R23274	Bovine parathyroid ho	1.82e+01
38	45	100.0	84 4	R23284	Bovine parathyroid ho	1.82e+01
39	45	100.0	84 4	R23513	Bovine parathyroid ho	1.82e+01
40	45	100.0	84 4	R23285	Bovine parathyroid ho	1.82e+01
41	45	100.0	84 4	R23413	Porcine parathyroid h	1.82e+01
42	45	100.0	84 4	R23280	Bovine parathyroid ho	1.82e+01
43	45	100.0	84 4	R23468	Porcine parathyroid h	1.82e+01
44	45	100.0	84 4	R21252	Human parathyroid hor	1.82e+01
45	45	100.0	115 1	P80305	Sequence of human par	1.82e+01

ALIGNMENTS

RESULT 1
ID R91656 Standard; peptide: 9 AA.
AC R91656;
DT 06-NOV-1996 (first entry)
DE Human parathyroid hormone antigenic peptide hPTH 9-17.
KW Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;
OS Synthesis; active hPTH 1-37.
PN DE4434551-AA.
PD 04-APR-1996.
PF 28-SEP-1994; 434551.
PR 28-SEP-1994; DE-434551.
PA (FORS.) FORSMANN W.
PI Adermann K, Forssmann W, Hock D, Maegerlein M;
DR WPI; 96-180391/19.
PT New antigenic peptide(s) from human parathyroid hormone - and
PT antibodies generated using them, able to distinguish between active
PT and inactive forms of the hormone
PS Claim 2; Page 5; 5pp; German.
CC The present sequence is a specific example of claimed immunogenic
CC peptides having a sequence from hPTH(1-37) which includes the N- or
CC C-terminal alpha-helical region and/or the non-structured region of
CC the hormone. Antibodies and their binding fragments generated by
CC injecting an animal with the peptides are useful as diagnostic
CC reagents for determination of biologically active hPTH(1-37).
SQ Sequence 9 AA.
Query Match 100.0%; Score 45; DB 18; length 9;
Best Local Similarity 100.0%; Pred. No. 1.82e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 hnlgrk 6
Qy 1 HNLGRK 6
RESULT 2
ID R88840 Standard; peptide: 32 AA.
AC R88840;
DT 07-OCT-1996 (first entry)
DE Human parathyroid hormone analogue, [Leu27]-hPTH(1-32)-NH2.
KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;
KW calcium regulation; reduced PKC activity; protein kinase C;

KW increased adenyl cyclase activity; cAMPase; bone loss.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT modified_site 32
 PN CA2126299-A. /note- "amidated"
 PD 21-DEC-1995.
 PE 20-JUN-1994; 126299.
 PR 20-JUN-1994; CA-126299.
 PA (WILL/) WILLICK G E.
 PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;
 PI WILLICK GE;
 DR WPI; 96-151754/16.
 PT New human parathyroid hormone analogues - which have increased
 PT adenyl cyclase activating activity, used for treating osteoporosis
 PS Claim 2; Page -, 21pp; English.
 CC R88829-R88841 are human parathyroid hormone (hPTH) analogues. The
 CC analogues increase G-protein coupled adenyl cyclase (cAMPase) activity and reduce protein kinase C (PKC) activity. The analogues can reverse the loss of bone and increase bone mass and density without undesirable effects. They are useful for the treatment of osteoporosis and other bone related disorders and disorders involving bone cell calcium regulation.
 CC
 SQ Sequence 32 AA;

Query Match 100.0%; Score 45; DB 18; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.82e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 9 hnlgrh 14
 |||||
 Oy 1 HNLGRH 6

Search completed: Thu Jul 30 10:33:53 1998
 Job time : 15 secs.

W I S E N H (TM)

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Masrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:33:02 1998; MasPar time 3.01 Seconds
Tabular output not generated. 72,782 Million cell updates/sec

Title: >US-08-817-547A-16
Description: (1-6) from US08817547A.pap
Perfect Score: 45
Sequence: 1 HNLGKH 6

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir56
1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 18.479; Variance 19.656; scale 0.940

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	45	100.0	34	5 12WG	parathyroid hormone 4	5.80e-01
2	45	100.0	34	5 12WF	parathyroid hormone 4	5.80e-01
3	45	100.0	34	5 12WE	parathyroid hormone (5.80e-01
4	45	100.0	34	5 12WA	parathyroid hormone (5.80e-01
5	45	100.0	35	5 12WD	parathyroid hormone (5.80e-01
6	45	100.0	36	5 12WB	parathyroid hormone (5.80e-01
7	45	100.0	37	5 12WH	parathyroid hormone (5.80e-01
8	45	100.0	37	5 12WC	parathyroid hormone (5.80e-01
9	45	100.0	105	2 IS1851	parathyroid hormone -	5.80e-01
10	45	100.0	115	2 JCA4202	parathyroid hormone -	5.80e-01
11	45	100.0	115	2 A05091	parathyroid hormone p	5.80e-01
12	45	100.0	115	1 PTHU	parathyroid hormone p	5.80e-01
13	45	100.0	115	1 PTHO	parathyroid hormone p	5.80e-01
14	45	100.0	115	1 PTHG	parathyroid hormone p	5.80e-01
15	45	95.6	1021	2 S44644	cyclic parathyroid ho	1.85e+00
16	42	93.3	34	5 12WH	parathyroid hormone -	3.28e+00
17	41	91.1	246	2 S01789	parathyroid hormone -	5.74e+00
18	40	88.9	172	2 A35145	parathyroid hormone -	9.97e+00
19	40	88.9	172	2 A35145	parathyroid hormone -	9.97e+00
20	39	86.7	264	2 A64637	parathyroid hormone -	1.72e+01
21	39	86.7	264	2 A64637	parathyroid hormone -	1.72e+01
22	39	86.7	480	1 A30065	parathyroid hormone -	1.72e+01
23	37	82.2	92	2 S41723	parathyroid hormone -	4.93e+01

24	37	82.2	116	2 A58566	nerve growth factor -	4.93e+01
25	37	82.2	116	1 NGNXXI	nerve growth factor -	4.93e+01
26	37	82.2	116	2 S13965	nerve growth factor -	4.93e+01
27	37	82.2	119	2 A34937	parathyroid hormone p	4.93e+01
28	37	82.2	232	2 I46679	parathyroid hormone p	4.93e+01
29	37	82.2	330	2 WNECH	alpha-smooth muscle a	4.93e+01
30	37	82.2	534	2 S61228	photosynthetic reacti	4.93e+01
31	37	82.2	633	2 JQ1242	DNA (cytosine-5'-)met	4.93e+01
32	37	82.2	1097	2 A29943	Viral replicase 2 - b	4.93e+01
33	37	82.2	1938	1 MMKM1	Toll protein precuro	4.93e+01
34	37	82.2	1947	1 S05697	myosin heavy chain D	4.93e+01
35	37	82.2	1966	1 MMKM1	myosin heavy chain C	4.93e+01
36	37	82.2	1969	1 S02771	myosin heavy chain B	4.93e+01
37	36	80.0	60	2 E69209	myosin heavy chain A	8.24e+01
38	36	80.0	123	2 S75382	conserved hypothetical	8.24e+01
39	36	80.0	130	2 B37059	hypothetical protein	8.24e+01
40	36	80.0	403	2 B69196	creatine kinase (EC 2	8.24e+01
41	36	80.0	540	1 OYHUCR	conserved hypothetical	8.24e+01
42	36	80.0	586	2 S73346	natriuretic peptide r	8.24e+01
43	36	80.0	700	2 JH0162	sn-glycerol-3-phospha	8.24e+01
44	36	80.0	933	2 S53523	No-on-transient A pro	8.24e+01
45	36	80.0	1209	2 A49440	methylentetrahydrofo	8.24e+01
					chromosome disjunctio	8.24e+01

ALIGNMENTS

RESULT	ENTRY	TITLE	12WG	#type complete
1	1	parathyroid hormone 4	37 mutant N-TERMINAL SUCCINYLATED -	
ALTERNATE_NAMES		n-succinyl-hp(4-37)		
PDB_TITLE		succinyl human parathyroid hormone 4-37, NMR, 10 structures		
ORGANISM		#formal_name synthetic		
REFERENCE		A67743		
#authors		Roesch, P.; Marx, U.C.		
#submission		submitted to the Brookhaven Protein Data Bank, June 1996		
#cross-references		PDB:12WG		
REFERENCE		TN003319		
#authors		Marx, U.C.		
#book		In Strukturen Verschiedener Parathormonfragmente in Loessung, pp. 0, Bayreuth : University of Bayreuth (Thesis), 1996		
COMMENT		Resolution: not applicable		
KEYWORDS		disease mutation; hormone; signal		
FEATURE				
2-9				
SUMMARY		#region helix (right hand alpha) \		
15-25		#region helix (right hand alpha) \		
		#length 34 #molecular-weight 4128 #checksum 5508		
Query Match		100.0%; Score 45; DB 5; Length 34;		
Best Local Similarity		100.0%; Pred. No. 5.80e-01;		
Matches		6; Conservative 0; Mismatches 0; Gaps 0;		
Db		6 HNLGKH 11		
Qy		1 HNLGKH 6		
RESULT		2		
ENTRY		12WF	#type complete	
TITLE		parathyroid hormone 4	37 mutant N-TERMINAL ACETYLATED -	
ALTERNATE_NAMES		n-acetyl-hp(4-37)		
PDB_TITLE		structure of n-terminal acetylated human parathyroid hormone,		
ORGANISM		NMR, 10 structures		
REFERENCE		#formal_name synthetic		
A67742				
#authors		Roesch, P.; Marx, U.C.		
#submission		submitted to the Brookhaven Protein Data Bank, June 1996		
#cross-references		PDB:12WF		
REFERENCE		TN003318		
#authors		Marx, U.C.		
#book		In Strukturen Verschiedener Parathormonfragmente in Loessung,		

Thu Jul 30 13:37:58 1998

US-08-817-547A-16.rpt

COMMENT Resolution: not applicable
pp.0, Bayreuth : University of Bayreuth (Thesis), 1996
KEYWORDS Determination: NMR
FEATURE disease mutation; hormone; signal
3-6 #region helix (right hand alpha)\
14-27 #region helix (right hand alpha)
SUMMARY #length 34 #molecular weight 4128 #checksum 5508
Query Match 100.0%; Score 45; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.80e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 6 HNLGRH 11
0Y 1 HNLGRH 6

Search completed: Thu Jul 30 10:33:20 1998
Job time : 18 secs.

MUSE

(TM)

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MSPrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:31:49 1998; MasPar time 2.04 Seconds
Tabular output not generated. 73.883 Million cell updates/sec

Title: >US-08-817-547A-16
Description: (1-6) from US08817547A.pep
Perfect Score: 45
Sequence: 1 HNLGKH 6

Scoring table:
PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues
Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 19.288; Variance 15.923; scale 1.211

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	45	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	4.76e-02
2	45	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	4.76e-02
3	45	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	4.76e-02
4	45	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	4.76e-02
5	45	100.0	115	1	PTHY_RAT PARATHYROID HORMONE PR	4.76e-02
6	45	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	4.76e-02
7	41	91.1	245	1	YPT7_CAELI HYPOTHETICAL 111.7 KD	2.00e-01
8	40	88.9	105	1	YBXE_SPAU PROBABLE RIBOSOMAL PRO	1.58e+00
9	40	88.9	171	1	PATA_BACSU PROTEIN SYNTHASE AND	1.58e+00
10	39	86.7	386	1	VC17_VACCC PROTEIN C17/B23	3.08e+00
11	39	86.7	480	1	PUTATIVE VENOM METALLO	3.08e+00
12	38	84.4	96	1	VPR_HVINS VPR PROTEIN (R ORF PRO	5.90e+00
13	38	84.4	614	1	YQ22_CAELI HYPOTHETICAL 69.0 KD P	5.90e+00
14	37	82.2	116	1	NGF_NAJAT NERVE GROWTH FACTOR (N	1.12e+01
15	37	82.2	116	1	NGF_NAJAT NERVE GROWTH FACTOR (N	1.12e+01
16	37	82.2	119	1	PTHY_CHICK PARATHYROID HORMONE PR	1.12e+01
17	37	82.2	308	1	PADI_SCHPO PADI PROTEIN	1.12e+01
18	37	82.2	330	1	RCEK_EKYSF REACTION CENTER PROTET	1.12e+01
19	37	82.2	1097	1	TOLC_DROME TOLC PROTEIN PRECURSOR	1.12e+01
20	37	82.2	1938	1	MYSD_CAELI MYOSIN HEAVY CHAIN C	1.12e+01
21	37	82.2	1947	1	MYSD_CAELI MYOSIN HEAVY CHAIN C	1.12e+01
22	37	82.2	1966	1	MYSB_CAELI MYOSIN HEAVY CHAIN B	1.12e+01
23	37	82.2	1969	1	MYSA_CAELI MYOSIN HEAVY CHAIN A	1.12e+01

RESULT	1	STANDARD	PRT	115 AA.	ALIGNMENTS		
AC	24	36	80.0	127	1	YAKH_RHISN HYPOTHETICAL 14.1 KD P	2.08e+01
AC	25	36	80.0	229	1	NEF_STVAG NEGATIVE FACTOR (F-PRO	2.08e+01
AC	26	36	80.0	381	1	KCRB_HUMAN CREATINE KINASE, B CHA	2.08e+01
AC	27	36	80.0	381	1	KCRB_CHICK CREATINE KINASE, B CHA	2.08e+01
AC	28	36	80.0	540	1	ANPC_HUMAN ATRIAL NATRIURETIC PEP	2.08e+01
AC	29	36	80.0	585	1	Y187_MYCGE HYPOTHETICAL ABC TRANS	2.08e+01
AC	30	36	80.0	586	1	Y187_MYCPN HYPOTHETICAL ABC TRANS	2.08e+01
AC	31	36	80.0	600	1	Y719_METUA HYPOTHETICAL ABC TRANS	2.08e+01
AC	32	36	80.0	700	1	RIP_HUMAN SERINE/THROMBIN PROT	2.08e+01
AC	33	36	80.0	700	1	NONA_DROME NO-ON-TRANSIENT A PROT	2.08e+01
AC	34	36	80.0	894	1	KDPD_ECOLI SENSOR PROTEIN KDPD (E	2.08e+01
AC	35	36	80.0	1063	1	DPOW_CLAPU PROBABLE DNA POLYMERAS	2.08e+01
AC	36	36	80.0	1147	1	SREL_HUMAN STEROL REGULATORY ELEM	2.08e+01
AC	37	36	80.0	1209	1	THR_DROME THREE ROWS PROTEIN	2.08e+01
AC	38	36	80.0	1357	1	YJ03_YEAST HYPOTHETICAL 154.9 KD	2.08e+01
AC	39	35	77.8	228	1	RL1_THETH 50S RIBOSOMAL PROTEIN	3.82e+01
AC	40	35	77.8	340	1	COND_NEUCR CONDITONATION-SPECIFIC P	3.82e+01
AC	41	35	77.8	415	1	ZN12_MICSA ZINC FINGER PROTEIN ZF	3.82e+01
AC	42	35	77.8	621	1	PLAK_MOUSE JUNCTION PLAKGLOBIN (3.82e+01
AC	43	35	77.8	829	1	GUTR_BACSU TRANSCRIPTION ACTIVATO	3.82e+01
AC	44	35	77.8	1371	1	PUR2_CHITE PHOSPHORIBOSYLAMINE--G	3.82e+01
AC	45	35	77.8	2437	1	NOTC_BRARE NEUROGENIC LOCUS NOTCH	3.82e+01
AC	21-JUL-1986	(REL. 01, CREATED)					
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)					
DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)					
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).						
GN	PTH.						
OS	BOS TAURUS (BOVINE).						
OC	EUFARYOTA, METAZOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA;						
OC	EUFARYOTA, ARTIODACTYLA.						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RP	MEDLINE: 80056617.						
RA	KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,						
RA	POTTS J.T. JR., RICH A.,						
RL	PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).						
RN	[2]						
RP	SEQUENCE FROM N.A.						
RP	MEDLINE: 82037785.						
RA	WEAVER C.A., GORDON D.F., KEMPER B.,						
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).						
RN	[3]						
RP	SEQUENCE FROM N.A.						
RP	MEDLINE: 83105964.						
RA	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.,						
RL	MOL. CELL. ENDOCRINOL. 28:411-424(1982).						
RN	[4]						
RP	SEQUENCE FROM N.A.						
RP	MEDLINE: 84262483.						
RA	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.,						
RL	GENE 28:319-329(1984).						
RN	[5]						
RP	SEQUENCE OF 26-115.						
RP	MEDLINE: 74142666.						
RA	HAMILTON J.W., NITALL H.D., JACOBS J.W., KEUTTMANN H.T., POTTS J.T. JR.,						
RA	COHN D.V.,						
RL	PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).						
RN	[6]						
RP	SEQUENCE OF 32-115.						
RP	MEDLINE: 71076162.						
RA	NITALL H.D., KEUTTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,						
RA	AUBBACH G.D., POTTS J.T. JR.,						
RL	HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970).						
RN	[7]						
RP	SEQUENCE OF 32-115.						
RP	MEDLINE: 71063634.						

Search completed: Thu Jul 30 10:31:56 1998
Job time : 7 secs.

RA BREWER H.B. JR., RONAN R.,
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE: 71091588.
RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
RA DEFLOS L.J., DAMSON B.F., HOGAN M.L., AUREACH G.D.,
RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL; J00023; G163641; -;
DR EMBL; J00024; G163643; -;
DR EMBL; J00024; E18249; ALT_SEQ.
DR EMBL; J00024; E18250; ALT_SEQ.
DR EMBL; K01938; G163647; -;
DR EMBL; M25082; G163645; -;
DR PIR; A01534; PTBO.
DR PIR; A24949; A24949.
DR PROSITE; PS00335; PARATHYROID; 1.
DR HORMONE; SIGNAL.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115
FT CONFLICT 106 106
SQ SEQUENCE 115 AA; 12980 MW; 673E45F2 CRC32;
V -> G (IN REF. 4).

Query Match

Best Local Similarity 100.0%; Score 45; DB 1; Length 115;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 40 HNLGKH 45
OY 1 HNLGKH 6

RESULT 2
ID PTH_CANFA STANDARD; PRT: 115 AA.
AC P52212;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.
OS CANIS FAMILIARIS (DOG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; CARNIVORA.
RN [1]
RA SEQUENCE FROM N.A.
RA TISSUE-PARATHYROID;
RA MEDLINE; 95369696.
RA ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,
RA DEWILLE J.W., CAPEN C.C.;
RL GENE 160:241-243(1995).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL; U15662; G558916; -;
DR PROSITE; PS00335; PARATHYROID; 1.
DR HORMONE; SIGNAL.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115
SQ SEQUENCE 115 AA; 12957 MW; 16ED0EBC CRC32;
BY SIMILARITY.
BY SIMILARITY.
PARATHYROID HORMONE.

Query Match

Best Local Similarity 100.0%; Score 45; DB 1; Length 115;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 40 HNLGKH 45
OY 1 HNLGKH 6

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RA SALMINEN M.O., KOCH C., SANDERS-BUELL E., EHRENBURG P.K.,
 RA MICHAEL N.L., CARR J.K., BURKE D.S., MCCUTCHAN F.E.,
 RL VIROLOGY 213:80-86(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NL4-3;
 RX MEDLINE; 86281827.
 RA ADACHI A., GENDELMAN H.E., KOENIG S., FOLKS T., WILLEY R.,
 RA RABSON A., MARTIN M.A.,
 RL J. VIROL. 59:284-291(1986).
 DR EMBL; D26942; G902802; -.
 FT CONFLICT 44 44 R -> O (IN REF. 2)
 SQ SEQUENCE 96 AA; 11391 MW; 035C4D75 CRC32;

Query Match 93.3%; Score 42; DB 11; Length 96;
 Best Local Similarity 83.3%; Pred.No. 8.18e-01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 40 HNLGRH 45
 1 HNLGRH 6

Search completed: Thu Jul 30 10:32:45 1998
 Job time : 33 secs.

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Msrch_dp protein - protein database search, using Smith-Waterman algorithm
 on: Thu Jul 30 10:36:04 1998; MasPar time 2.57 Seconds
 29.790 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-817-547A-17
 Description: (1-5) from US08817547A.pep
 Perfect Score: 36
 Sequence: 1 HNLGK 5

Scoring table:
 PAM 150
 Gap 15

Searched: 124785 segs, 15338987 residues
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-geneseq31-2
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27

Statistics: Mean 12.815; Variance 28.014; scale 0.457

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description	Pred. No.
1	36	100.0	34	26	R62432	Accelerator peptide b
2	36	100.0	34	9	R58189	[F23,H25,H26,L27,I28,
3	36	100.0	34	8	R41568	[Lys15,16 His27]hPTH
4	36	100.0	34	9	R58187	[Phe23,His25,His26,Le
5	36	100.0	34	7	R34455	Bovine parathyroid ho
6	36	100.0	34	7	R34457	Human parathyroid ho
7	36	100.0	34	22	W17958	Human parathyroid hor
8	36	100.0	34	22	W17953	Human parathyroid hor
9	36	100.0	34	22	W17957	Human parathyroid hor
10	36	100.0	35	14	R74490	Parathyroid hormone p
11	36	100.0	35	14	R74489	Parathyroid hormone p
12	36	100.0	36	9	R58060	[L8,Al6,Q18,A19,R22]
13	36	100.0	36	9	R58055	[L8,Q18]-hPTH(1-36)-C
14	36	100.0	36	9	R58186	[Ala18]-hPTH(1-36)-NH
15	36	100.0	38	9	R58163	[Pro33]-hPTH(1-38)-OH
16	36	100.0	38	9	R58165	[Ile33]-hPTH(1-38)-OH
17	36	100.0	38	9	R58061	[Ile33]-hPTH(1-38)-OH
18	36	100.0	38	9	R58147	[His22]-hPTH(1-38)-OH
19	36	100.0	38	9	R58126	[Ala19]-hPTH(1-38)-OH

20	36	100.0	38	9	R58124	[Lys19]-hPTH(1-38)-OH	1.04e+02
21	36	100.0	38	9	R58105	[Val14]-hPTH(1-38)-OH	1.04e+02
22	36	100.0	38	9	R58108	[Arg14]-hPTH(1-38)-OH	1.04e+02
23	36	100.0	38	9	R58077	[Leu33]-hPTH(1-38)-OH	1.04e+02
24	36	100.0	38	9	R58078	[Gly33]-hPTH(1-38)-OH	1.04e+02
25	36	100.0	44	26	P30015	Human parathyroid hor	1.04e+02
26	36	100.0	84	27	W25687	Human parathyroid hor	1.04e+02
27	36	100.0	84	4	R23430	Porcine parathyroid h	1.04e+02
28	36	100.0	84	4	R23263	Bovine parathyroid ho	1.04e+02
29	36	100.0	84	4	R23422	Porcine parathyroid h	1.04e+02
30	36	100.0	84	4	R23413	Porcine parathyroid h	1.04e+02
31	36	100.0	84	8	R42069	Stability-enhanced hu	1.04e+02
32	36	100.0	84	5	R29562	Oxidation resistant p	1.04e+02
33	36	100.0	84	5	R29561	Oxidation resistant p	1.04e+02
34	36	100.0	84	4	R23367	Bovine parathyroid ho	1.04e+02
35	36	100.0	84	4	R23349	Bovine parathyroid ho	1.04e+02
36	36	100.0	84	4	R23393	Porcine parathyroid h	1.04e+02
37	36	100.0	84	4	R23274	Bovine parathyroid ho	1.04e+02
38	36	100.0	84	4	R23274	Bovine parathyroid ho	1.04e+02
39	36	100.0	84	4	R23261	Porcine parathyroid h	1.04e+02
40	36	100.0	84	4	R21162	Human parathyroid hor	1.04e+02
41	36	100.0	84	4	R21163	Human parathyroid hor	1.04e+02
42	36	100.0	84	4	R23477	Porcine parathyroid h	1.04e+02
43	36	100.0	84	4	R23476	Porcine parathyroid h	1.04e+02
44	36	100.0	84	4	R23405	Porcine parathyroid h	1.04e+02
45	36	100.0	84	4	R23297	Bovine parathyroid ho	1.04e+02

ALIGNMENTS

RESULT 1	ID	R62432	standard; peptide; 34 AA.
AC	R62432;		
DT	31-JUL-1995	(first entry)	
DE	Accelerator peptide basic region peptide, p-8.		
KW	Accelerator; basic amino acid; cell growth factor; growth; gingiva;		
KW	periodontal tissue; regeneration; periodontitis; periodontal pocket;		
KW	down growth; epithelium; fibre adhesion; cement.		
OS	Synthetic.		
PN	J06234653-A.		
PD	23-AUG-1994.		
PF	10-FEB-1993; 045998.		
PR	10-FEB-1993; JP-045998.		
PA	(SUNZ) SUNSTAR CHEM IND CO LTD.		
DR	WPI: 95-157631/21.		
PT	Accelerator for regenerating periodontal tissue - comprises		
PT	peptide having 3-34 aminoacid residues having connected basic		
PT	aminoacid residues		
PS	Disclosure, Page 3: 7pp; Japanese.		
CC	The sequences in R62425-36 are peptide fragments of an accelerator		
CC	protein which contain at least two basic amino acids. The accelerator		
CC	also comprises a cell growth factor. The accelerator may be used to		
CC	accelerate the growth of periodontal tissue regeneration. The		
CC	accelerator is applied by opening the gingiva, treating the tissue		
CC	destroyed by periodontitis and applying the accelerator in the		
CC	epithelium pocket. The accelerator reduces the down growth of the		
CC	periodontal and accelerates fibre adhesion and regenerates cement.		
CC	Sequence 34 AA:		
QY	Query Match	100.0%; Score 36; Length 34;	
QY	Best Local Similarity 100.0%; Pred. No. 1.04e+02;		
QY	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 hnlkg 13		
QY			
QY	1 HNLGK 5		
RESULT 2	ID	R58189	standard; peptide; 34 AA.
AC	R58189;		
DT	20-SEP-1994	(first entry)	
DE	[F23,H25,H26,L27,I28,A29,E30,I31,T33,A34]-hPTH(1-34)-NH2.		

KW Human parathyroid hormone; hPTH; variant; analogue;
 KW calcium; depletion; fixation; resorption; osteoporosis;
 KW hypoparathyroidism.
 OS Synthetic.
 FH Key
 FT modified_site 34 Location/Qualifiers
 PN GB2269176-A.
 PD 02-FEB-1994.
 PF 12-JUL-1994.
 PR 15-JUL-1993; 014384.
 PR 18-DEC-1992; GB-015009.
 PR 23-DEC-1992; GB-026415.
 PR 23-DEC-1992; GB-026859.
 PR 28-JAN-1993; GB-001691.
 PR 28-JAN-1993; GB-001692.
 PR 14-APR-1993; GB-007673.
 PR 19-APR-1993; GB-008033.
 PA (SANO) SANDOZ LTD.
 (BAUE/) BAUER W.
 (SANO) SANDOZ PATENT GMBH.
 (SANO) SANDOZ-ERFINDUNGEN VERW GMS MBH.
 PI Albert R. Bauer W., Breckenridge R., Cardinaux F.
 PI Gombert P., Gram H., Lewis I., Ramage P., Schneider H.
 DR WPI: 94-018352/03.
 PT New active para-thyroid hormone variants - used for treating or
 preventing osteoporosis etc.
 PS Example 187; Page 44; 92pp; English.
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 SQ Sequence 34 AA;

Query Match
 Best Local Similarity 100.0%; Score 36; DB 9; Length 34;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 9 hnlgk 13
 Qy 1 hnlgk 5

Search completed: Thu Jul 30 10:36:20 1998
 Job time : 16 secs.

W E S E R I E S
(TM)

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MPsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:35:29 1998; MasPar time 2.99 Seconds
61.109 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-17
Description: (1-5) from US08817547A.pep
Perfect Score: 36
Sequence: 1 HNLGK 5

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plf56
1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 17.484; Variance 16.519; scale 1.058

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description	Pred. No.
1	36	100.0	34	5 12WG	parathyroid hormone 4	1.89e+01
2	36	100.0	34	5 12WF	parathyroid hormone 4	1.89e+01
3	36	100.0	34	5 12WE	parathyroid hormone (1.89e+01
4	36	100.0	34	5 12WA	parathyroid hormone (1.89e+01
5	36	100.0	35	5 12WD	parathyroid hormone (1.89e+01
6	36	100.0	35	5 12WB	parathyroid hormone (1.89e+01
7	36	100.0	37	5 12WH	parathyroid hormone (1.89e+01
8	36	100.0	37	5 12WC	parathyroid hormone (1.89e+01
9	36	100.0	105	2 151851	parathyroid hormone -	1.89e+01
10	36	100.0	115	1 PRPG	parathyroid hormone -	1.89e+01
11	36	100.0	115	2 JCA4202	parathyroid hormone -	1.89e+01
12	36	100.0	115	2 A05091	parathyroid hormone p	1.89e+01
13	36	100.0	115	1 PTHO	parathyroid hormone p	1.89e+01
14	36	100.0	115	1 PTHO	parathyroid hormone p	1.89e+01
15	36	100.0	123	2 S75382	parathyroid hormone p	1.89e+01
16	36	100.0	894	2 B42372	hypothetical protein	1.89e+01
17	36	100.0	1097	2 J00301	regulatory protein Kd	1.89e+01
18	36	100.0	1172	2 S42622	hypothetical 127k pro	1.89e+01
19	36	100.0	1209	2 A49440	three rows protein -	1.89e+01
20	36	94.4	142	2 C70059	chromosome disjunctio	6.05e+01
21	34	94.4	146	1 HBHY	hypothetical protein	6.05e+01
22	34	94.4	146	1 HB02	hemoglobin beta chain	6.05e+01
23	34	94.4	146	2 J00163	hemoglobin beta chain	6.05e+01

24	34	94.4	147	2	S22336	hemoglobin beta chain	6.05e+01
25	34	94.4	314	2	G66818	CMP-binding factor ho	6.05e+01
26	34	94.4	348	2	F69831	iron(III) dicitrate-b	6.05e+01
27	34	94.4	412	1	RNECTA	tRNA adenylyltransfer	6.05e+01
28	34	94.4	416	2	B64132	tRNA adenylyltransfer	6.05e+01
29	34	94.4	573	1	HHRT60	chaperonin groEL prec	6.05e+01
30	34	94.4	573	1	A32800	chaperonin groEL prec	6.05e+01
31	34	94.4	573	1	HHMS60	chaperonin groEL prec	6.05e+01
32	34	94.4	573	1	A34173	mitochondrial protein	6.05e+01
33	34	94.4	711	2	E69953	hypothetical protein	6.05e+01
34	34	94.4	759	2	G69258	ATP-dependent RNA hel	6.05e+01
35	34	94.4	830	2	C69011	conserved hypothetical	6.05e+01
36	34	94.4	1021	2	S44644	F37A4.7 protein - Cae	6.05e+01
37	34	94.4	3135	2	A46584	transmission-blocking	6.05e+01
38	33	91.7	34	5	1H7H	cyclic parathyroid ho	1.06e+02
39	33	91.7	146	1	HBOL	hemoglobin beta chain	1.06e+02
40	33	91.7	147	1	HBMS	hemoglobin beta major	1.06e+02
41	33	91.7	147	2	S34719	hemoglobin beta-2.0 c	1.06e+02
42	33	91.7	273	5	1ORDA	quinone-reductase (EC	1.06e+02
43	33	91.7	273	5	1QKDB	quinone-reductase (EC	1.06e+02
44	33	91.7	274	2	152851	NAD(P)H dehydrogenase	1.06e+02
45	33	91.7	578	2	E69259	aldehyde ferredoxin o	1.06e+02

ALIGNMENTS

RESULT	1	12WG	#type complete
ENTRY	parathyroid hormone 4	37 mutant N-TERMINAL SUCCINYLATED -	
TITLE	synthetic		
ALTERNATE_NAMES	n-succinyl-hpnh(4-37)		
PDB_TITLE	succinyl human parathyroid hormone 4-37, NMR, 10 structures		
ORGANISM	#formal_name synthetic		
REFERENCE	A67743		
#authors	Roesch, P.; Marx, U.C.		
#submission	submitted to the Brookhaven Protein Data Bank, June 1996		
#cross-references	PDB:12WG		
REFERENCE	TN003319		
#book	Marx, U.C.		
COMMENT	In Strukturen Verschiedener Parathormonfragmente in Loessung,		
COMMENT	pp.0, Bayreuth : University of Bayreuth (Thesis), 1996		
KEYWORDS	Resolution: not applicable		
FEATURE	disease mutation: hormone; signal		
SUMMARY	#region helix (right hand alpha) \		
2-9	#region helix (right hand alpha)		
15-25	#length 34 #molecular-weight 4128 #checksum 5508		
Query Match	100.0%; Score 36; DB 5; Length 34;		
Best Local Similarity	100.0%; Pred. No. 1.89e+01;		
Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
DB	6 HNLGK 10		
QY	1 HNLGK 5		
RESULT	2	12WF	#type complete
ENTRY	parathyroid hormone 4	37 mutant N-TERMINAL ACETYLATED -	
TITLE	synthetic		
ALTERNATE_NAMES	n-acetyl-hpnh(4-37)		
PDB_TITLE	structure of n-terminal acetylated human parathyroid hormone,		
ORGANISM	NMR, 10 structures		
REFERENCE	#formal_name synthetic		
A67742	Roesch, P.; Marx, U.C.		
#authors	submitted to the Brookhaven Protein Data Bank, June 1996		
#submission	submitted to the Brookhaven Protein Data Bank, June 1996		
#cross-references	PDB:12WF		
REFERENCE	TN003318		
#book	Marx, U.C.		
In Strukturen Verschiedener Parathormonfragmente in Loessung,			

COMMENT pp.0, Bayreuth : University of Bayreuth (Thesis), 1996
 COMMENT Resolution: not applicable
 KEYWORDS Determination: NMR
 FEATURE disease mutation; hormone; signal
 3-6
 14-27
 SUMMARY #region helix (right hand alpha) \
 #region helix (right hand alpha) \
 #length 34 #molecular-weight 4128 #checksum 5508
 Query Match 100.0%; Score 36; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.89e+01;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 6 HNLGK 10
 QY 1 HNLGK 5
 Search completed: Thu Jul 30 10:35:46 1998
 CPU time : 17 secs.

WIDEORIT (TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:34:11 1998; MasPar time 2.00 Seconds
Tabular output not generated. 62.590 Million cell updates/sec

Title: >US-08-817-547A-17
Description: (1-5) from US08817547A.pep
Perfect Score: 36
Sequence: 1 HNLGK 5

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 18.208; Variance 13.355; scale 1.363

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	36	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	3.42e+00
2	36	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	3.42e+00
3	36	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	3.42e+00
4	36	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	3.42e+00
5	36	100.0	115	1	PTHY_RAT PARATHYROID HORMONE PR	3.42e+00
6	36	100.0	894	1	KDPD_ECOLI SENSOR PROTEIN KDPD (E	3.42e+00
7	36	100.0	1063	1	DPOK_CAPU PROBABLE DNA POLYMERAS	3.42e+00
8	36	100.0	1209	1	THR_DROME THREE ROWS PROTEIN..	3.42e+00
9	36	100.0	146	1	HHB_ONDZI HEMOGLOBIN BETA CHAIN..	1.41e+01
10	36	100.0	146	1	HHB_MESAU HEMOGLOBIN BETA-MAJOR	1.41e+01
11	36	100.0	146	1	HHB_MESAU HEMOGLOBIN BETA-MAJOR	1.41e+01
12	36	100.0	146	1	HHB_MESAU HEMOGLOBIN BETA-MAJOR	1.41e+01
13	36	100.0	146	1	HHB_MESAU HEMOGLOBIN BETA-MAJOR	1.41e+01
14	36	100.0	146	1	HHB_MESAU HEMOGLOBIN BETA-MAJOR	1.41e+01
15	36	100.0	146	1	HHB_MESAU HEMOGLOBIN BETA-MAJOR	1.41e+01
16	36	100.0	146	1	HHB_MESAU HEMOGLOBIN BETA-MAJOR	1.41e+01
17	36	100.0	146	1	HHB_MESAU HEMOGLOBIN BETA-MAJOR	1.41e+01
18	36	100.0	146	1	HHB_MESAU HEMOGLOBIN BETA-MAJOR	1.41e+01
19	36	100.0	146	1	HHB_MESAU HEMOGLOBIN BETA-MAJOR	1.41e+01
20	36	100.0	146	1	HHB_MESAU HEMOGLOBIN BETA-MAJOR	1.41e+01
21	36	100.0	146	1	HHB_MESAU HEMOGLOBIN BETA-MAJOR	1.41e+01
22	36	100.0	146	1	HHB_MESAU HEMOGLOBIN BETA-MAJOR	1.41e+01
23	36	100.0	146	1	HHB_MESAU HEMOGLOBIN BETA-MAJOR	1.41e+01

24	33	91.7	146	1	HHB2_RAT HEMOGLOBIN BETA CHAIN..	2.78e+01
25	33	91.7	146	1	HHB2_MITCA HEMOGLOBIN BETA CHAIN..	2.78e+01
26	33	91.7	146	1	HHB2_SPECI HEMOGLOBIN BETA CHAIN..	2.78e+01
27	33	91.7	146	1	HHB1_RAT HEMOGLOBIN BETA CHAIN..	2.78e+01
28	33	91.7	146	1	HHB2_MOUSE HEMOGLOBIN BETA-2 CHAI	2.78e+01
29	33	91.7	146	1	HHB2_MOUSE HEMOGLOBIN BETA-2 CHAI	2.78e+01
30	33	91.7	146	1	HHB2_MOUSE HEMOGLOBIN BETA-2 CHAI	2.78e+01
31	33	91.7	146	1	HHB2_MOUSE HEMOGLOBIN BETA-2 CHAI	2.78e+01
32	33	91.7	146	1	HHB2_MOUSE HEMOGLOBIN BETA-2 CHAI	2.78e+01
33	33	91.7	146	1	HHB2_MOUSE HEMOGLOBIN BETA-2 CHAI	2.78e+01
34	33	91.7	146	1	HHB2_MOUSE HEMOGLOBIN BETA-2 CHAI	2.78e+01
35	33	91.7	146	1	HHB2_MOUSE HEMOGLOBIN BETA-2 CHAI	2.78e+01
36	33	91.7	146	1	HHB2_MOUSE HEMOGLOBIN BETA-2 CHAI	2.78e+01
37	33	91.7	146	1	HHB2_MOUSE HEMOGLOBIN BETA-2 CHAI	2.78e+01
38	33	91.7	146	1	HHB2_MOUSE HEMOGLOBIN BETA-2 CHAI	2.78e+01
39	33	91.7	146	1	HHB2_MOUSE HEMOGLOBIN BETA-2 CHAI	2.78e+01
40	33	91.7	146	1	HHB2_MOUSE HEMOGLOBIN BETA-2 CHAI	2.78e+01
41	33	91.7	146	1	HHB2_MOUSE HEMOGLOBIN BETA-2 CHAI	2.78e+01
42	33	91.7	146	1	HHB2_MOUSE HEMOGLOBIN BETA-2 CHAI	2.78e+01
43	33	91.7	146	1	HHB2_MOUSE HEMOGLOBIN BETA-2 CHAI	2.78e+01
44	33	91.7	146	1	HHB2_MOUSE HEMOGLOBIN BETA-2 CHAI	2.78e+01
45	33	91.7	146	1	HHB2_MOUSE HEMOGLOBIN BETA-2 CHAI	2.78e+01

ALIGNMENTS

RESULT	ID	PTHY_BOVIN	STANDARD;	PTHY	115 AA.
AC	P01268;				
DT	21-JUL-1986 (REL. 01, CREATED)				
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).				
GN	PTH.				
OS	BOS TAURUS (BOVINE).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; ARTIODACTYLA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	WEAVER C.A., GORDON D.F., KEMPER B.;				
RA	MOL. CELL. ENDOCRINOL. 28:411-424(1982).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RA	WEAVER C.A., GORDON D.F., KEMPER B.;				
RA	MOL. CELL. ENDOCRINOL. 28:411-424(1982).				
RN	[5]				
RP	SEQUENCE OF 26-115.				
RA	HAMILTON J.W., NATAL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,				
RA	COHN D.V.;				
RA	PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).				
RN	[6]				
RP	SEQUENCE OF 32-115.				
RA	NATAL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,				
RA	AURBACH G.D., POTTS J.T. JR.;				
RA	HOPPE-SELYER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).				
RN	[7]				
RP	SEQUENCE OF 32-115.				
RA	MEDLINE; 71063634.				

RA BREWER H.B., JR., ROMAN R.,
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE: 71091588.
RA POTTS J.T., JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
RA DEFLOS L.J., DAWSON B.F., HOGAN M.L., AUBACH G.D.,
RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL: V00106; G85; -.
DR EMBL: J00023; G163641; -.
DR EMBL: J00024; G163643; -.
DR EMBL: J00024; E18249; ALT_SEQ.
DR EMBL: J00024; E18250; ALT_INIT.
DR EMBL: K01938; G163647; -.
DR EMBL: M25082; G163645; -.
DR PIR: A01534; PTBO.
DR PIR: A24949; A24949.
DR PROSITE: PS00335; PARATHYROID; 1.
CC HORMONE; SIGNAL.
FT PROPEP 1 25
FT CHAIN 26 31
FT CONFLICT 32 115 PARATHYROID HORMONE.
V -> G (IN REF. 4).
SQ SEQUENCE 115 AA; 12980 MM; 673EA5F2 CRC32;

Query Match 100.0%; Score 36; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 3,42e+00;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 40 HNLGR 44
QY 1 HNLGR 5

RESULT 2
ID ID PTH_PIG STANDARD; PRT; 115 AA.
AC P01269;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.
OS SUS SCROFA (PIG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLA.
RN [1]
NA SEQUENCE FROM N.A.
NA SCHMELZER H.-J., GROSS G., WIDERA G., MAYER H.;
RL NUCLEIC ACIDS RES. 15:6740-6740(1987).
RN [2]
RP SEQUENCE OF 26-115.
RX MEDLINE: 76018954.
RA CHU L.L.H., HUANG W.-Y., LITLEDIKE E.T., HAMILTON J.W., COHN D.V.;
RL BIOCHEMISTRY 14:3631-3635(1975).
RN [3]
RP SEQUENCE OF 32-115.
RX MEDLINE: 7425317.
RA SAUER R.T., NIALL H.D., HOGAN M.L., KEUTMANN H.T., O'RIORDAN J.L.H.,
RA POTTS J.T., JR.;
RL BIOCHEMISTRY 13:1994-1999(1974).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL: X05722; G1839; -.
DR PIR: B26806; B26806.
DR PIR: B26806; B26806.
DR PROSITE: PS00335; PARATHYROID; 1.
KW HORMONE; SIGNAL.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 PARATHYROID HORMONE.

SQ SEQUENCE 115 AA; 12852 MM; 98B67FA7 CRC32;

Query Match 100.0%; Score 36; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 3,42e+00;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 40 HNLGR 44
QY 1 HNLGR 5

Search completed: Thu Jul 30 10:34:18 1998
Job time : 7 secs.

N I P S E R E I

(TM)

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Search: protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:34:37 1998; Maspar time 3.52 Seconds
Tabular output not generated. 59.805 Million cell updates/sec

Title: >US-08-817-547A-17
Description: (1-5) from US08817547A.pep
Perfect Score: 36
Sequence: 1 HNLGK 5

Scoring table: PAM 150
Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: streptmb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 17.545; Variance 13.620; scale 1.288

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	36	100.0	105 10	063473	PARATHYROID HORMONE (F	5.59e+00
2	36	100.0	123 9	P95954	ORF C04013.	5.59e+00
3	36	100.0	517 8	041520	LIPXYGENASE (FRAGMENT	5.59e+00
4	36	100.0	659 9	041074	ER LUMENAL CHAPERONE B	5.59e+00
5	36	100.0	1209 3	094525	THREE ROWS PROTEIN.	5.59e+00
6	34	94.4	142 9	007624	YWIA, SBO, YWIB, ARGS	2.24e+01
7	34	94.4	242 2	015383	CC3 (CC3).	2.24e+01
8	34	94.4	314 9	007521	HYPOTHETICAL 35.7 KD P	2.24e+01
9	34	94.4	327 12	042357	RETINAL HOMEOBOX PROTE	2.24e+01
10	34	94.4	348 9	007616	HYPOTHETICAL 38.6 KD P	2.24e+01
11	34	94.4	573 10	P97602	60 KD CHAPERONIN (PROT	2.24e+01
12	34	94.4	759 9	030165	ATP-DEPENDENT RNA HELI	2.24e+01
13	34	94.4	830 9	027158	CONSERVED PROTEIN.	2.24e+01
14	34	94.4	3134 3	025994	RANSMISSION-BLOCKING T	2.24e+01
15	33	91.7	51 3	027366	RHOPTRY PROTEIN (FRAM	4.37e+01
16	33	91.7	96 11	063223	RAT HEMOGLOBIN BETA-CH	4.37e+01
17	33	91.7	146 10	063011	VPR PROTEIN.	4.37e+01
18	33	91.7	147 10	063011	ZERO BETA-1 GLOBIN.	4.37e+01
19	33	91.7	147 10	062669	ZERO BETA-1 GLOBIN.	4.37e+01
20	33	91.7	147 10	062670	0 BETA-2 GLOBIN.	4.37e+01

RESULT	ID	Score	Query Match	Length	DB ID	Description	Pred. No.
1	063473	100.0%	36	105	AA.	PARATHYROID HORMONE (F	5.59e+00
2	P95954	94.4%	34	123	9	ORF C04013.	5.59e+00
3	041520	94.4%	36	517	8	LIPXYGENASE (FRAGMENT	5.59e+00
4	041074	94.4%	36	659	9	ER LUMENAL CHAPERONE B	5.59e+00
5	094525	94.4%	36	1209	3	THREE ROWS PROTEIN.	5.59e+00
6	007624	94.4%	34	142	9	YWIA, SBO, YWIB, ARGS	2.24e+01
7	015383	94.4%	34	242	2	CC3 (CC3).	2.24e+01
8	007521	94.4%	34	314	9	HYPOTHETICAL 35.7 KD P	2.24e+01
9	042357	94.4%	34	327	12	RETINAL HOMEOBOX PROTE	2.24e+01
10	007616	94.4%	34	348	9	HYPOTHETICAL 38.6 KD P	2.24e+01
11	P97602	94.4%	34	573	10	60 KD CHAPERONIN (PROT	2.24e+01
12	030165	94.4%	34	759	9	ATP-DEPENDENT RNA HELI	2.24e+01
13	027158	94.4%	34	830	9	CONSERVED PROTEIN.	2.24e+01
14	025994	94.4%	34	3134	3	RANSMISSION-BLOCKING T	2.24e+01
15	027366	91.7%	33	51	3	RHOPTRY PROTEIN (FRAM	4.37e+01
16	063223	91.7%	33	96	11	RAT HEMOGLOBIN BETA-CH	4.37e+01
17	063011	91.7%	33	146	10	VPR PROTEIN.	4.37e+01
18	063011	91.7%	33	147	10	ZERO BETA-1 GLOBIN.	4.37e+01
19	062669	91.7%	33	147	10	ZERO BETA-1 GLOBIN.	4.37e+01
20	062670	91.7%	33	147	10	0 BETA-2 GLOBIN.	4.37e+01

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	DB ID	Description	Pred. No.
1	063473	100.0%	36	105	AA.	PARATHYROID HORMONE (F	5.59e+00
2	P95954	94.4%	34	123	9	ORF C04013.	5.59e+00
3	041520	94.4%	36	517	8	LIPXYGENASE (FRAGMENT	5.59e+00
4	041074	94.4%	36	659	9	ER LUMENAL CHAPERONE B	5.59e+00
5	094525	94.4%	36	1209	3	THREE ROWS PROTEIN.	5.59e+00
6	007624	94.4%	34	142	9	YWIA, SBO, YWIB, ARGS	2.24e+01
7	015383	94.4%	34	242	2	CC3 (CC3).	2.24e+01
8	007521	94.4%	34	314	9	HYPOTHETICAL 35.7 KD P	2.24e+01
9	042357	94.4%	34	327	12	RETINAL HOMEOBOX PROTE	2.24e+01
10	007616	94.4%	34	348	9	HYPOTHETICAL 38.6 KD P	2.24e+01
11	P97602	94.4%	34	573	10	60 KD CHAPERONIN (PROT	2.24e+01
12	030165	94.4%	34	759	9	ATP-DEPENDENT RNA HELI	2.24e+01
13	027158	94.4%	34	830	9	CONSERVED PROTEIN.	2.24e+01
14	025994	94.4%	34	3134	3	RANSMISSION-BLOCKING T	2.24e+01
15	027366	91.7%	33	51	3	RHOPTRY PROTEIN (FRAM	4.37e+01
16	063223	91.7%	33	96	11	RAT HEMOGLOBIN BETA-CH	4.37e+01
17	063011	91.7%	33	146	10	VPR PROTEIN.	4.37e+01
18	063011	91.7%	33	147	10	ZERO BETA-1 GLOBIN.	4.37e+01
19	062669	91.7%	33	147	10	ZERO BETA-1 GLOBIN.	4.37e+01
20	062670	91.7%	33	147	10	0 BETA-2 GLOBIN.	4.37e+01

RL MOL. MICROBIOL. 22:175-191(1996).
 DR EMBL: Y08257; E283828;
 SQ SEQUENCE 123 AA; 14021 MW; 316E0391 CRC32;
 Query Match 100.0%; Score 36; DB 9; Length 123;
 Best Local Similarity 100.0%; Pred. No. 5.59e+00;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 6 HNLGK 10
 QY 1 HNLGK 5

Search completed: Thu Jul 30 10:35:11 1998
 Job time : 34 secs.

[W][O][R][D]

(TW)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:38:52 1998; MasPar time 2.75 Seconds
Tabular output not generated. 78.050 Million cell updates/sec

Title: >US-08-817-547A-18
Description: (1-14) from US08817547A.pep
Perfect Score: 103
Sequence: 1 LRKKLDVHNFVAL 14

Scoring table: PAM 150
Gap 15

Searched: 124785 segs, 15338987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 19.363; Variance 67.336; scale 0.288

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	103	100.0	38	9	R58283	[Trp(Pmc)23]-hPTH(1-3	1.80e-03
2	103	100.0	38	9	R58151	[Ser22]-hPTH(1-38)-OH	1.80e-03
3	103	100.0	38	9	R58134	[Ile19]-hPTH(1-38)-OH	1.80e-03
4	103	100.0	38	9	R58133	[Asp19]-hPTH(1-38)-OH	1.80e-03
5	103	100.0	38	9	R58138	[Ala21]-hPTH(1-38)-OH	1.80e-03
6	103	100.0	38	9	R58137	[Phe20]-hPTH(1-38)-OH	1.80e-03
7	103	100.0	44	26	P30015	Human parathyroid hor	1.80e-03
8	103	100.0	47	25	W21946	Fusion protein compri	1.80e-03
9	103	100.0	84	27	W25687	Human parathyroid hor	1.80e-03
10	103	100.0	84	4	R23837	Porcine parathyroid h	1.80e-03
11	103	100.0	84	4	R23262	Bovine parathyroid ho	1.80e-03
12	103	100.0	84	4	R21188	Human parathyroid hor	1.80e-03
13	103	100.0	84	4	R21189	Human parathyroid hor	1.80e-03
14	103	100.0	84	4	R21156	Human parathyroid hor	1.80e-03
15	103	100.0	84	4	R21157	Human parathyroid hor	1.80e-03
16	103	100.0	84	4	R23429	Porcine parathyroid h	1.80e-03
17	103	100.0	84	4	R23259	Bovine parathyroid ho	1.80e-03
18	103	100.0	84	4	R23384	Porcine parathyroid h	1.80e-03
19	103	100.0	84	4	R23246	Human parathyroid hor	1.80e-03

20	103	100.0	84	4	R21223	Human parathyroid hor	1.80e-03
21	103	100.0	84	4	R21222	Human parathyroid hor	1.80e-03
22	103	100.0	84	4	R23265	Bovine parathyroid ho	1.80e-03
23	103	100.0	84	4	R23441	Porcine parathyroid h	1.80e-03
24	103	100.0	84	4	R21240	Human parathyroid hor	1.80e-03
25	103	100.0	84	25	W29420	Human parathyroid hor	1.80e-03
26	103	100.0	84	4	R23317	Bovine parathyroid ho	1.80e-03
27	103	100.0	84	4	R23415	Porcine parathyroid h	1.80e-03
28	103	100.0	84	4	R23241	Human parathyroid hor	1.80e-03
29	103	100.0	84	4	R23378	Human parathyroid hor	1.80e-03
30	103	100.0	84	4	R23237	Human parathyroid hor	1.80e-03
31	103	100.0	84	4	R21192	Human parathyroid hor	1.80e-03
32	103	100.0	84	4	R23439	Porcine parathyroid h	1.80e-03
33	103	100.0	84	4	R21227	Human parathyroid hor	1.80e-03
34	103	100.0	84	4	R23258	Bovine parathyroid ho	1.80e-03
35	103	100.0	84	4	R21168	Human parathyroid hor	1.80e-03
36	103	100.0	84	4	R23290	Bovine parathyroid ho	1.80e-03
37	103	100.0	84	4	R23402	Porcine parathyroid h	1.80e-03
38	103	100.0	84	4	R23275	Bovine parathyroid ho	1.80e-03
39	103	100.0	84	4	R23394	Porcine parathyroid h	1.80e-03
40	103	100.0	84	4	R23299	Bovine parathyroid ho	1.80e-03
41	103	100.0	84	4	R23326	Bovine parathyroid ho	1.80e-03
42	103	100.0	84	4	R23344	Bovine parathyroid ho	1.80e-03
43	103	100.0	84	4	R23313	Bovine parathyroid ho	1.80e-03
44	103	100.0	84	4	R23449	Porcine parathyroid h	1.80e-03
45	103	100.0	115	2	P80275	Sequence of human pre	1.80e-03

ALIGNMENTS

RESULT 1
ID R58283 standard; peptide; 38 AA.
AC R58283;
DT 20-SEP-1994 (first entry)
DE [Trp(Pmc)23]-hPTH(1-38)-NH2.
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
FH Key location/Qualifiers
FT modified_site 23 /label=Other
FT /note="Trp(Pmc) where Pmc is
FT 2,5,7,8-Pentamethylchroman-6-sulphonyl."
FT modified_site 38
FT FT /note="In amide form"
PN modified_site 38
PN FT
PN FT
PD GB2269176-A.
PD 02-FEB-1994.
PF 12-JUL-1993; 014384.
PR 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (SANO) SANDOZ LTD.
PA (BAUER) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F,
PI Gombert F, Gram H, Lewis I, Ramage F, Schneider H,
PI Waelchli R, Rainer A;
DR WPI: 94-018352/03.
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 281; Page 46; 92pp; English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption. In cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.

SQ Sequence 38 AA:

Query Match

Best Local Similarity 100.0%; Score 103; DB 9; Length 38;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 lrrklgdyhmfval 37

QY 1 LRRKLDVHNFVAL 14

RESULT 2

ID R58151 standard; peptide; 38 AA.

AC R58151;

DT 20-SEP-1994 (first entry)

DE [Ser22]-hPTH(1-38)-OH.

KW Human parathyroid hormone; hPTH; variant; analogue;

KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;

KW hypoparathyroidism.

KW Synthetic.

GB269176-A.

02-FEB-1994.

PF 12-JUL-1993; 014384.

PR 15-JUL-1992; GB-015009.

PR 18-DEC-1992; GB-026415.

PR 23-DEC-1992; GB-026859.

PR 23-DEC-1992; GB-026861.

PR 28-JAN-1993; GB-001691.

PR 28-JAN-1993; GB-001692.

PR 14-APR-1993; GB-007673.

PR 19-APR-1993; GB-008033.

PA (SANO) SANDOZ LTD.

PA (BAUE/) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-EREINDINGEN VERW GES MBH.

PI Albert R, Bauer W, Breckenridge R, Cardinaux F,

PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

PI Waelchli R, Rainer A;

DR MPI; 94-018352/03.

PT New active para-thyroid hormone variants - used for treating or

PT preventing osteoporosis etc.

PS Example 149; Page 40; 92pp; English.

CC This peptide is an example of a highly generic formula covering

CC parathyroid hormone variants useful for treating or preventing bone

CC conditions associated with calcium depletion/resorption, in cases

CC where calcium fixation is required (esp. osteoporosis) or to treat

CC hypoparathyroidism.

SQ Sequence 38 AA:

Query Match

Best Local Similarity 100.0%; Score 103; DB 9; Length 38;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 lrrklgdyhmfval 37

QY 1 LRRKLDVHNFVAL 14

Search completed: Thu Jul 30 10:39:16 1998
Job time : 24 secs.

N O T E S
(TM)

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MPsrch_PP protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:38:07 1998; MasPar time 3.41 Seconds
Tabular output not generated. 150.175 Million cell updates/sec

Title: >US-08-817-547A-18
Description: (1-14) from US08817547A.pep
Perfect Score: 103
Sequence: 1 LRRKLDVHNHVAL 14

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr56
1:plr1 2:plr2 3:plr3 4:plr4 5:nrl3d

Statistics: Mean 26.838; Variance 43.748; scale 0.613

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	103	100.0	34	5	12WE parathyroid hormone (8.54e-08	
2	103	100.0	34	5	12WG parathyroid hormone (8.54e-08	
3	103	100.0	34	5	12WF parathyroid hormone 4 8.54e-08	
4	103	100.0	35	5	12WD parathyroid hormone (8.54e-08	
5	103	100.0	36	5	12WB parathyroid hormone (8.54e-08	
6	103	100.0	37	5	12WC parathyroid hormone (8.54e-08	
7	103	100.0	37	5	12WB parathyroid hormone (8.54e-08	
8	103	100.0	115	2	12WC parathyroid hormone (8.54e-08	
9	103	100.0	115	2	12WB parathyroid hormone (8.54e-08	
10	103	100.0	115	1	12WB parathyroid hormone (8.54e-08	
11	103	100.0	115	1	12WB parathyroid hormone (8.54e-08	
12	101	98.1	115	2	12WB parathyroid hormone (8.54e-08	
13	91	88.3	105	2	12WB parathyroid hormone (8.54e-08	
14	84	81.6	34	5	12WB parathyroid hormone (8.54e-08	
15	84	81.6	34	5	12WB parathyroid hormone (8.54e-08	
16	66	64.1	2475	2	S35307 polypeptide hormone (7.59e-01	
17	64	62.1	444	2	S09681 citrate transport pro 1.64e+00	
18	61	59.2	462	2	A42401 macrophage elastase (5.05e+00	
19	58	56.3	183	2	S42547 glucose-1-phosphate a 1.51e+01	
20	58	56.3	313	1	00ECIL hypothetical 34.6K pr 1.51e+01	
21	58	56.3	330	1	151545 myc protein - African 1.51e+01	
22	58	56.3	419	1	TXYLWC transforming protein 1.51e+01	
23	58	56.3	2843	1	RBUHAP adenomatous polyposis 1.51e+01	

24	58	56.3	2845	2	149505	adenomatous polyposis 1.51e+01
25 <td>57</td> <td>55.3</td> <td>281</td> <td>2</td> <td>S41854 phosphoprotein phosph 2.15e+01</td> <td></td>	57	55.3	281	2	S41854 phosphoprotein phosph 2.15e+01	
26 <td>57</td> <td>55.3</td> <td>470</td> <td>2</td> <td>A49499 metalloelastase HME (2.15e+01</td> <td></td>	57	55.3	470	2	A49499 metalloelastase HME (2.15e+01	
27 <td>57</td> <td>55.3</td> <td>525</td> <td>2</td> <td>C64313 hypothetical protein 2.15e+01</td> <td></td>	57	55.3	525	2	C64313 hypothetical protein 2.15e+01	
28 <td>57</td> <td>55.3</td> <td>555</td> <td>2</td> <td>S69641 hypothetical protein 2.15e+01</td> <td></td>	57	55.3	555	2	S69641 hypothetical protein 2.15e+01	
29 <td>56<td>54.4</td><td>208</td><td>2</td><td>S20583 DNA-directed RNA poly 3.06e+01</td><td></td></td>	56 <td>54.4</td> <td>208</td> <td>2</td> <td>S20583 DNA-directed RNA poly 3.06e+01</td> <td></td>	54.4	208	2	S20583 DNA-directed RNA poly 3.06e+01	
30 <td>56<td>54.4</td><td>445</td><td>2</td><td>S43452 surface antigen - hep 3.06e+01</td><td></td></td>	56 <td>54.4</td> <td>445</td> <td>2</td> <td>S43452 surface antigen - hep 3.06e+01</td> <td></td>	54.4	445	2	S43452 surface antigen - hep 3.06e+01	
31 <td>56<td>54.4</td><td>477</td><td>1</td><td>KCRITR stromelysin I (EC 3.4 3.06e+01</td><td></td></td>	56 <td>54.4</td> <td>477</td> <td>1</td> <td>KCRITR stromelysin I (EC 3.4 3.06e+01</td> <td></td>	54.4	477	1	KCRITR stromelysin I (EC 3.4 3.06e+01	
32 <td>56<td>54.4</td><td>477</td><td>1</td><td>KCMS61 stromelysin I (EC 3.4 3.06e+01</td><td></td></td>	56 <td>54.4</td> <td>477</td> <td>1</td> <td>KCMS61 stromelysin I (EC 3.4 3.06e+01</td> <td></td>	54.4	477	1	KCMS61 stromelysin I (EC 3.4 3.06e+01	
33 <td>56<td>54.4</td><td>478</td><td>1</td><td>KCRBS1 stromelysin I (EC 3.4 3.06e+01</td><td></td></td>	56 <td>54.4</td> <td>478</td> <td>1</td> <td>KCRBS1 stromelysin I (EC 3.4 3.06e+01</td> <td></td>	54.4	478	1	KCRBS1 stromelysin I (EC 3.4 3.06e+01	
34 <td>56<td>54.4</td><td>608</td><td>2</td><td>A46312 gag polyprotein - hum 3.06e+01</td><td></td></td>	56 <td>54.4</td> <td>608</td> <td>2</td> <td>A46312 gag polyprotein - hum 3.06e+01</td> <td></td>	54.4	608	2	A46312 gag polyprotein - hum 3.06e+01	
35 <td>56<td>54.4</td><td>651</td><td>2</td><td>G64058 DNA topoisomerase (EC 3.06e+01</td><td></td></td>	56 <td>54.4</td> <td>651</td> <td>2</td> <td>G64058 DNA topoisomerase (EC 3.06e+01</td> <td></td>	54.4	651	2	G64058 DNA topoisomerase (EC 3.06e+01	
36 <td>56<td>54.4</td><td>752</td><td>1</td><td>C2HU complement C2 precurs 3.06e+01</td><td></td></td>	56 <td>54.4</td> <td>752</td> <td>1</td> <td>C2HU complement C2 precurs 3.06e+01</td> <td></td>	54.4	752	1	C2HU complement C2 precurs 3.06e+01	
37 <td>56<td>53.4</td><td>102</td><td>2</td><td>S53076 probable membrane pro 4.33e+01</td><td></td></td>	56 <td>53.4</td> <td>102</td> <td>2</td> <td>S53076 probable membrane pro 4.33e+01</td> <td></td>	53.4	102	2	S53076 probable membrane pro 4.33e+01	
38 <td>55<td>53.4</td><td>119</td><td>2</td><td>A34937 parathyroid hormone p 4.33e+01</td><td></td></td>	55 <td>53.4</td> <td>119</td> <td>2</td> <td>A34937 parathyroid hormone p 4.33e+01</td> <td></td>	53.4	119	2	A34937 parathyroid hormone p 4.33e+01	
39 <td>55<td>53.4</td><td>203</td><td>2</td><td>S20584 DNA-directed RNA poly 4.33e+01</td><td></td></td>	55 <td>53.4</td> <td>203</td> <td>2</td> <td>S20584 DNA-directed RNA poly 4.33e+01</td> <td></td>	53.4	203	2	S20584 DNA-directed RNA poly 4.33e+01	
40 <td>55<td>53.4</td><td>227</td><td>2</td><td>A24911 prolactin-like protei 4.33e+01</td><td></td></td>	55 <td>53.4</td> <td>227</td> <td>2</td> <td>A24911 prolactin-like protei 4.33e+01</td> <td></td>	53.4	227	2	A24911 prolactin-like protei 4.33e+01	
41 <td>55<td>53.4</td><td>284</td><td>2</td><td>S74516 dimethyladenosine tra 4.33e+01</td><td></td></td>	55 <td>53.4</td> <td>284</td> <td>2</td> <td>S74516 dimethyladenosine tra 4.33e+01</td> <td></td>	53.4	284	2	S74516 dimethyladenosine tra 4.33e+01	
42 <td>55<td>53.4</td><td>453</td><td>2</td><td>S59456 hypothetical protein 4.33e+01</td><td></td></td>	55 <td>53.4</td> <td>453</td> <td>2</td> <td>S59456 hypothetical protein 4.33e+01</td> <td></td>	53.4	453	2	S59456 hypothetical protein 4.33e+01	
43 <td>55<td>53.4</td><td>692</td><td>2</td><td>A34548 follitropin receptor 4.33e+01</td><td></td></td>	55 <td>53.4</td> <td>692</td> <td>2</td> <td>A34548 follitropin receptor 4.33e+01</td> <td></td>	53.4	692	2	A34548 follitropin receptor 4.33e+01	
44 <td>55<td>53.4</td><td>911</td><td>2</td><td>S28098 ste6 protein - fission 4.33e+01</td><td></td></td>	55 <td>53.4</td> <td>911</td> <td>2</td> <td>S28098 ste6 protein - fission 4.33e+01</td> <td></td>	53.4	911	2	S28098 ste6 protein - fission 4.33e+01	
45 <td>55<td>53.4</td><td>1634</td><td>2</td><td>JC5500 phosphoinositide 3-ki 4.33e+01</td><td></td></td>	55 <td>53.4</td> <td>1634</td> <td>2</td> <td>JC5500 phosphoinositide 3-ki 4.33e+01</td> <td></td>	53.4	1634	2	JC5500 phosphoinositide 3-ki 4.33e+01	

ALIGNMENTS

RESULT	1	12WE	#type complete
ENTRY	1	parathyroid hormone (residues 4-37) - human	
TITLE		HPTH(4-37)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 4-37, NMR 10	
PDB_TITLE		structures	
ORGANISM		.#formal_name Homo sapiens #common_name man	
REFERENCE		A67860	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WE	
REFERENCE		TN001721	
#authors		Marx, U.C.	
#book		In Struktur und Verschleuder Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996	
COMMENT		Resolution: not applicable	
COMMENT		Determination: NMR	
KEYWORDS		hormone	
FEATURE			
15-25			
SUMMARY		#region helix (right hand alpha)	
		length 34 #molecular-weight 4128 #checksum 5508	
Query Match		100.0%; Score 103; DB 5; Length 34;	
Best Local Similarity		100.0%; Pred. No. 8.54e-08;	
Matches		14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	21	LRRKLDVHNHVAL 34	
QY	1	LRRKLDVHNHVAL 14	
RESULT	2	12WG	#type complete
ENTRY		parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -	
TITLE		synthetic	
ALTERNATE_NAMES		n-succinyl-hPTH(4-37)	
PDB_TITLE		succinyl human parathyroid hormone 4-37, NMR, 10 structures	
ORGANISM		#formal_name synthetic	
REFERENCE		A67743	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WG	
REFERENCE		TN003319	
#authors		Marx, U.C.	
#book		In Struktur und Verschleuder Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996	
COMMENT		Resolution: not applicable	

```

COMMENT      Determination: NMR
KEYWORDS     disease mutation; hormone; signal
FEATURE      2-9      #region helix (right hand alpha)\
                15-25  #region helix (right hand alpha)
SUMMARY      #length 34 #molecular-weight 4128 #checksum 5508

Query Match  100.0%; Score 103; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 8.54e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 21 LKKKLDVHNFFVAL 34
QY 1 LKKKLDVHNFFVAL 14

Search completed: Thu Jul 30 10:38:34 1998
Job time : 27 secs.

```

WATERMAN
(TW)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:36:38 1998; MasPar time 2.28 Seconds
153.724 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-18
Description: (1-14) from US08817547A.pep
Perfect Score: 103
Sequence: 1 LRRKIDVHNFVAL 14

Scoring table:
PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 28.165; Variance 35.949; scale 0.783

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	103	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	1.98e-10
2	103	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	1.98e-10
3	103	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	1.98e-10
4	103	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	1.98e-10
5	101	98.1	115	1	PTHY_RAT PARATHYROID HORMONE PR	6.31e-10
6	64	62.1	444	1	CITR_KLEPN CITRATE-PROTON SYMPORT	2.04e-01
7	61	59.2	462	1	MACROPHAGE METALLOELAS	8.06e-01
8	58	56.3	184	1	GLG2_ARATH GLUCOSE-1-PHOSPHATE AD	3.03e+00
9	58	56.3	313	1	RIBP_ECOLI RIBOPHOSPHATE KINASE (EC	3.03e+00
10	58	56.3	419	1	MYC1_XENLA MYC 1 PROTO-ONCOGENE P	3.03e+00
11	58	56.3	2843	1	ADENOMATOUS POLYPOSIS	3.03e+00
12	57	55.3	281	1	PZC1_YEAST PROTEIN PHOSPHATASE 2C	4.66e+00
13	57	55.3	470	1	MACROPHAGE METALLOELAS	4.66e+00
14	57	55.3	525	1	Y107_METJA HYPOTHETICAL PROTEIN M	4.66e+00
15	56	54.4	475	1	COG3_MOUSE STROMELYSIN-1 PRECURSOR	7.13e+00
16	56	54.4	477	1	COG3_MOUSE STROMELYSIN-1 PRECURSOR	7.13e+00
17	56	54.4	478	1	COG3_RABIT STROMELYSIN-1 PRECURSOR	7.13e+00
18	56	54.4	636	1	RPOC_CTAPA DNA-DIRECTED RNA POLYI	7.13e+00
19	56	54.4	651	1	TOP3_HAEIN DNA TOPOISOMERASE IIII	7.13e+00
20	56	54.4	752	1	CO2_HUMAN COMPLEMENT C2 PRECURSOR	7.13e+00
21	55	53.4	102	1	YMB8_YEAST VERY HYPOTHETICAL 11.8	1.08e+01
22	55	53.4	119	1	PTHY_CHICK PARATHYROID HORMONE PR	1.08e+01
23	55	53.4	162	1	Y4XD_HHISN HYPOTHETICAL 18.0 KD P	1.08e+01

ID	PTHY_CANFA	STANDARD:	PRT:	115 AA.		
24	55	53.4	203	1	RPOC_PROHO DNA-DIRECTED RNA POLYM	1.08e+01
25	55	53.4	227	1	PRRA_RAT PLACENTAL PROLACTIN-LI	1.08e+01
26	55	53.4	305	1	HLYE_ECOLI HEMOLYSIN E (HEMOLYSIN	1.08e+01
27	55	53.4	447	1	KCC2_YEAST CALCIUM/CALMODULIN-DEP	1.08e+01
28	55	53.4	692	1	FSHR_RAT FOLLICLE STIMULATING H	1.08e+01
29	55	53.4	693	1	FSHR_CHICK FOLLICLE STIMULATING H	1.08e+01
30	55	53.4	911	1	STES_SCHRO STE6 PROTEIN	1.08e+01
31	55	53.4	1053	1	UBA3_WHEAT UBQUITIN-ACTIVATING E	1.08e+01
32	54	52.4	130	1	FLTS_HUMAN FILLENSIN (LENS FIBER C	1.64e+01
33	54	52.4	154	1	V17K_SSVL HYPOTHETICAL 17.8 KD P	1.64e+01
34	54	52.4	189	1	VNOO_YEAST VERY HYPOTHETICAL 21.7	1.64e+01
35	54	52.4	233	1	DP3E_BUCAP DNA POLYMERASE III, EP	1.64e+01
36	54	52.4	379	1	KAPO_BOVIN CAMP-DEPENDENT PROTEIN	1.64e+01
37	54	52.4	379	1	KAPO_BOVIN CAMP-DEPENDENT PROTEIN	1.64e+01
38	54	52.4	380	1	KAPO_RAT CAMP-DEPENDENT PROTEIN	1.64e+01
39	54	52.4	381	1	KAPO_HUMAN CAMP-DEPENDENT PROTEIN	1.64e+01
40	54	52.4	421	1	SYS_TRETH SERIL-TRNA SYNTHETASE	1.64e+01
41	54	52.4	687	1	FSHR_EQUUS FOLLICLE STIMULATING H	1.64e+01
42	54	52.4	694	1	FSHR_HORSE FOLLICLE STIMULATING H	1.64e+01
43	54	52.4	752	1	HPRI_YEAST HPRI PROTEIN.	1.64e+01
44	54	52.4	926	1	KINH_NEUCR KININ HEAVY CHAIN.	1.64e+01
45	54	52.4	3344	1	POLG_PRSVH GENOME POLYPROTEIN (CO	1.64e+01

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	115 AA.
ID	PTHY_CANFA			
AC	P52212;			
DT	01-OCT-1996 (REL. 34, CREATED)			
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).			
GN	PTH.			
OS	CANIS FAMILIARIS (DOG).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; CARNIVORA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-PARATHYROID.			
RX	MEDLINE; 95369696.			
RA	ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,			
RA	DEWILLE J.W., CAPEN C.C.,			
RL	GENE 160:241-243(1995).			
CC	-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN			
CC	BONE AND PREVENTING THEIR RENAL EXCRETION.			
DR	EMBL; U15662; G558916; -.			
DR	PROSITE; PS00335; PARATHYROID.1.			
KW	HORMONE; SIGNAL.			
FT	SIGNAL.			
FT	PROPEP			
FT	CHAIN			
SQ	SEQUENCE			
Query Match	100.0%;	Score 103;	DB 1;	Length 115;
Best Local Similarity	100.0%;	Pred. No. 1.98e-10;		
Matches	14;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	
DB	55 LRRKIDVHNFVAL 68			
Qy	1 LRRKIDVHNFVAL 14			
RESULT	2	STANDARD:	PRT:	115 AA.
ID	PTHY_BOVIN			
AC	P01268;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).			
GN	PTH.			
OS	BOS TAURUS (BOVINE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			

Search completed: Thu Jul 30 10:36:46 1998
Job time : 8 secs.

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OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 80056617.
RA KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
RN [2]
RL PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
RP SEQUENCE FROM N.A.
RX MEDLINE; 82037785.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RN [3]
RL PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
RP SEQUENCE FROM N.A.
RX MEDLINE; 83105964.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RN [4]
RL MOL. CELL. ENDOCRINOL. 28:411-424(1982).
RP SEQUENCE FROM N.A.
RX MEDLINE; 84262483.
RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
RN [5]
RL GENE 28:319-329(1984).
RP SEQUENCE OF 26-115.
RX MEDLINE; 74142666.
RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,
RN [6]
RL PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
RP SEQUENCE OF 32-115.
RX MEDLINE; 71076162.
RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,
RN [7]
RL AURBACH G.D., POTTS J.T. JR.;
RP HOPPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).
RX MEDLINE; 71063634.
RA BREWER H.B. JR., RONAN R.;
RN [8]
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RP SYNTHESIS OF 32-65.
RX MEDLINE; 71091588.
RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
RN [9]
RL DEFLOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;
RP PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
DR BONE AND PREVENTING THEIR RENAL EXCRETION.
EMBL; J00106; G85; -
EMBL; J00023; G163641; -
EMBL; J00024; G163643; -
EMBL; J00024; E18249; ALT_SEQ.
EMBL; J00024; E18250; ALT_SEQ.
EMBL; K01938; G163647; -
EMBL; M25082; G163645; -
DR PIR; A01534; PTBO.
DR PIR; A24949; A24949.
DR PROSITE; PS00335; PARATHYROID; 1.
DR KW HORMONE; SIGNAL.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 PARATHYROID HORMONE.
FT CONFLICT 106 106 V -> G (IN REF. 4).
SQ SEQUENCE 115 AA; 12980 MW; 673EAF2 CRC32;

Query Match 100.0%; Score 103; DB 1; Length 115;
Best local Similarity 100.0%; Pred. No. 1.98e-10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 55 LRRKLDVHNFFVAL 68
QY 1 LRRKLDVHNFFVAL 14
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M105E161
(TM)

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Msrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:37:03 1998; Maspar time 4.02 Seconds
146.589 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-18
Description: (1-14) from US08817547A.pep
Perfect Score: 103
Sequence: 1 LRRKLDVHNFVAL 14

Scoring table: PAM 150
Gap 15

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 26.844; Variance 35.900; scale 0.748

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	91	88.3	105	10	PARATHYROID HORMONE (F	3.26e+07
2	66	64.1	2475	11	POLYPROTEIN PP220.	1.09e+01
3	61	59.2	207	11	ORF36L.	1.07e+00
4	61	59.2	342	11	SIMILAR TO BACTERIOPHA	1.07e+00
5	59	57.3	320	9	HYPOTHEICAL PROTEIN I	3.97e+00
6	58	56.3	228	9	COSMID F56F4.	3.97e+00
7	58	56.3	330	12	MYC PROTEIN (FRAGMENT	3.97e+00
8	58	56.3	591	3	F52E10.5 (FRAGMENT)	3.97e+00
9	58	56.3	1291	2	MRNA (K1A0067) FOR OR	3.97e+00
10	58	56.3	2743	2	POLYPOSIS LOCUS-ENCODE	3.97e+00
11	58	56.3	2829	12	ADENOMATOUS POLYPOSIS	3.97e+00
12	58	56.3	2842	10	APC PROTEIN.	3.97e+00
13	58	56.3	2844	2	POLYPOSIS LOCUS-ENCODE	3.97e+00
14	58	56.3	2845	10	ADENOMATOUS POLYPOSIS	3.97e+00
15	57	55.3	299	3	SIMILAR TO SER/THR PRO	6.09e+00
16	57	55.3	355	1	D8035.17P.	6.09e+00
17	57	55.3	688	10	FOLICILE-STIMULATING H	6.09e+00
18	56	54.4	1077	8	UBIQUITIN-ACTIVATING E	9.30e+00
19	56	54.4	445	11	PRE-S-S ORF.	9.30e+00
20	56	54.4	477	4	MATRIX METALLOPROTEIN	9.30e+00

RESULT	ID	PRELIMINARY	PRT	105 AA.		
21	56	54.4	752	2	COMPLEMENT COMPONENT C	9.30e+00
22	56	54.4	1080	8	UBIQUITIN-ACTIVATING E	9.30e+00
23	55	53.4	231	1	CAM KINASE II (FRAGMEN	1.41e+01
24	55	53.4	245	8	PURATIVE MADS-BOX FAMI	1.41e+01
25	55	53.4	8	039296	AGL15 TYPE 2.	1.41e+01
26	55	53.4	284	9	DIMETHYLADEOSINE TRAN	1.41e+01
27	55	53.4	395	3	ALLERGEN (CR-PII).	1.41e+01
28	55	53.4	453	1	HYPOTHEICAL 50.0 KD P	1.41e+01
29	55	53.4	693	12	OVARIAN FOLLICLE-STIMU	1.41e+01
30	55	53.4	821	9	GLYCOCEN PHOSPHORYLASE	1.41e+01
31	55	53.4	1167	10	ZINC FINGER PROTEIN (F	1.41e+01
32	55	53.4	1186	10	ZINC FINGER PROTEIN 10	1.41e+01
33	55	53.4	1459	3	ROSE10.5.	1.41e+01
34	55	53.4	1634	2	PHOSPHOINOSITIDE 3-KIN	1.41e+01
35	55	53.4	2401	3	HOPTRY PROTEIN (FRAGM	1.41e+01
36	55	53.4	2708	3	CHLOROQUINE RESISTANCE	1.41e+01
37	55	53.4	2742	3	CHLOROQUINE RESISTANCE	1.41e+01
38	55	53.4	2819	3	STRAIN HB3 CG2 (CG2).	1.41e+01
39	54	52.4	465	10	MACROPHAGE METALLOELAS	2.13e+01
40	54	52.4	694	3	K06G2.6. PROTEIN.	2.13e+01
41	54	52.4	735	3	C06G3.9. PROTEIN.	2.13e+01
42	54	52.4	962	9	HYPOTHEICAL 104.6 KD	2.13e+01
43	54	52.4	993	3	VINCULIN.	2.13e+01
44	54	52.4	3344	11	PREV YK POLYPROTEIN.	2.13e+01
45	54	52.4	4162	12	CONNECTIN/TITIN (FRAGM	2.13e+01

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	105 AA.
AC	063473			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE (FRAGMENT).			
GN	PTH.			
OS	RATUUS NORVEGICUS (RAT).			
OC	EUKARYOTA; METAFOA; CHORDATA; VERTEBRATA; MAMMALIA;			
OC	EUROTERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TTSUB-THYROID, AND PARATHYROID;			
RA	SCHMELZER H.J., GROSS G., MAYER H.;			
RL	ADV. GENE TECHNOL. 21:228-229(1984).			
DR	EMBL; M54875; G601933; -			
FT	NON TER			
SO	SEQUENCE	105 AA;	11746 MW;	6AC3163E CRC32;
DB	45	LRRKLDVHNFVAL	58	
OY	1	LRRKLDVHNFVAL	14	
RESULT	2	PRELIMINARY	PRT;	2475 AA.
AC	008358			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)			
DE	POLYPROTEIN PP220.			
GN	CP2475L.			
OS	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V) (ASFV).			
OC	VRIDAE; DS-DNA NONENVELOPED VIRUSES; IRIDOVIRIDAE.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 93327788.			
RA	SIMON-MATEO C.; ANDRES G.; VINUELA E.;			
RL	EMBO J. 12:2977-2987(1993).			

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RN [2]
RP COMPLETE GENOME.
RA YANEZ R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,
RA RODRIGUEZ J.F., VINUELA E.;
RL VIROLOGY 208:249-278(1995).
CC -1- FUNCTION: POLYPROTEIN PP220 IS THE PRECURSOR OF THE MAJOR VIRION
CC PROTEINS P150, P37, P34 AND P14 OF AFRICAN SWINE FEVER VIRUS.
DR EMBL: Z222777; G394709; -
DR EMBL: U18466; G780461; -
KW POLYPROTEIN.
SQ SEQUENCE 2475 AA; 281479 MW; 6F4E3C0A CRC32;

Query Match 64.1%; Score 66; DB 11; Length 2475;
Best Local Similarity 75.0%; Pred. No. 1.09e-01;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 1944 LRKTLQDVISFY 1955
QY 1 LRKRLQDVHNFV 12

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Search completed: Thu Jul 30 10:37:48 1998
 Job time : 45 secs.

WORLDWIDE
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:41:57 1998; MasPar time 2.73 Seconds
Tabular output not generated. 73.134 Million cell updates/sec

Title: >US-08-817-547A-19
Description: (1-13) from US08817547A.pep
Perfect Score: 95
Sequence: 1 RKKLQDVHNFVAL 13

Scoring table:
PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 18.828; Variance 67.821; scale 0.278

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	95	100.0	38	9 R58123	[Ser19]-hPTH(1-38)-OH	1.55e-02
2	95	100.0	38	9 R58134	[Ile19]-hPTH(1-38)-OH	1.55e-02
3	95	100.0	38	9 R58018	Isopropyl-Llys(IsoPro	1.55e-02
4	95	100.0	38	9 R58138	[Ala21]-hPTH(1-38)-OH	1.55e-02
5	95	100.0	38	9 R58137	[Phe20]-hPTH(1-38)-OH	1.55e-02
6	95	100.0	38	9 R58124	[Lys19]-hPTH(1-38)-OH	1.55e-02
7	95	100.0	44	26 P30015	Human parathyroid hor	1.55e-02
8	95	100.0	47	25 W21946	Fusion protein compri	1.55e-02
9	95	100.0	84	27 W25687	Human parathyroid hor	1.55e-02
10	95	100.0	84	4 R23500	Porcine parathyroid h	1.55e-02
11	95	100.0	84	4 R23540	Bovine parathyroid ho	1.55e-02
12	95	100.0	84	4 R23387	Porcine parathyroid h	1.55e-02
13	95	100.0	84	4 R23262	Bovine parathyroid ho	1.55e-02
14	95	100.0	84	4 R21188	Human parathyroid hor	1.55e-02
15	95	100.0	84	4 R21189	Human parathyroid hor	1.55e-02
16	95	100.0	84	4 R23415	Porcine parathyroid h	1.55e-02
17	95	100.0	84	4 R23317	Bovine parathyroid ho	1.55e-02
18	95	100.0	84	4 R23429	Porcine parathyroid h	1.55e-02
19	95	100.0	84	4 R23359	Bovine parathyroid ho	1.55e-02

20	95	100.0	84	4 R23384	Porcine parathyroid h	1.55e-02
21	95	100.0	84	4 R23246	Human parathyroid hor	1.55e-02
22	95	100.0	84	4 R21184	Human parathyroid hor	1.55e-02
23	95	100.0	84	4 R21156	Human parathyroid hor	1.55e-02
24	95	100.0	84	4 R21157	Human parathyroid hor	1.55e-02
25	95	100.0	84	4 R23242	Human parathyroid hor	1.55e-02
26	95	100.0	84	4 R21240	Human parathyroid hor	1.55e-02
27	95	100.0	84	25 W29420	Human parathyroid hor	1.55e-02
28	95	100.0	84	4 R21169	Human parathyroid hor	1.55e-02
29	95	100.0	84	4 R23241	Human parathyroid hor	1.55e-02
30	95	100.0	84	4 R23501	Porcine parathyroid h	1.55e-02
31	95	100.0	84	4 R23237	Human parathyroid hor	1.55e-02
32	95	100.0	84	4 R21192	Human parathyroid hor	1.55e-02
33	95	100.0	84	4 R21164	Human parathyroid hor	1.55e-02
34	95	100.0	84	4 R21227	Human parathyroid hor	1.55e-02
35	95	100.0	84	4 R23258	Bovine parathyroid ho	1.55e-02
36	95	100.0	84	4 R21168	Human parathyroid hor	1.55e-02
37	95	100.0	84	4 R23290	Bovine parathyroid ho	1.55e-02
38	95	100.0	84	4 R23402	Porcine parathyroid h	1.55e-02
39	95	100.0	84	4 R23275	Bovine parathyroid ho	1.55e-02
40	95	100.0	84	4 R23394	Porcine parathyroid h	1.55e-02
41	95	100.0	84	4 R23326	Bovine parathyroid ho	1.55e-02
42	95	100.0	84	7 R34452	Bovine parathyroid ho	1.55e-02
43	95	100.0	84	4 R21211	Human parathyroid hor	1.55e-02
44	95	100.0	84	4 R23449	Porcine parathyroid h	1.55e-02
45	95	100.0	115	2 P80275	Sequence of human pre	1.55e-02

ALIGNMENTS

RESULT 1
ID R58123 standard; peptide; 38 AA.
AC R58123;
DT 20-SEP-1994 (first entry)
DE [Ser19]-hPTH(1-38)-OH.
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
PN GB269176-A.
PD 02-FEB-1994.
PF 12-JUL-1993; 014384.
PR 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (SANO) SANDOZ LTD.
PA (BAUE) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F,
PI Gombert F, Gram H, Lewis I, Ramege P, Schneider H;
PI Waelchli R, Rainer A;
DR WPI: 94-018352/03.
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 120; Page 39; 92pp; English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 38 AA.
Query Match 100.0%; Score 95; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.55e-02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 25 rkkldqvhmfval 37

QY 1 RKKLQDVHNFVAL 13

RESULT

2
ID R58134 standard; peptide; 38 AA.
AC R58134:
DT 20-SEP-1994 (first entry)
DE [11e19]-hPTH(1-38)-OH.
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
PN GB2269176-A.
PD 02-FEB-1994.
PF 12-JUL-1993.
PR 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
28-JAN-1993; GB-001691.
28-JAN-1993; GB-001692.
14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (SANO) SANDOZ LTD.
PA (BAUE/) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PI (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Waelchli R, Rainer A;
DR WPI; 94-018352/03
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 131; Page 40; 92pp; English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 38 AA;

Query Match 100.0%; Score 95; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. NO. 1.55e-02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 25 rklqdvhnfvnl 37
1 RKKLQDVHNFVAL 13

Search completed: Thu Jul 30 10:42:20 1998
Job time : 23 secs.

(五)

COMMENT Determination: NMR
 KEYWORDS disease mutation; hormone; signal
 FEATURE
 2-9 #region helix (right hand alpha)\
 15-25 #region helix (right hand alpha)
 SUMMARY #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 95; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.06e-07;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 22 RKKLDVHNFEVAL 34
 0Y 1 RKKLDVHNFEVAL 13

Search completed: Thu Jul 30 10:41:40 1998
 Job time : 27 secs.

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(TM)

MPsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:39:34 1998; Maspar time 2.25 Seconds
Tabular output not generated. 145.141 Million cell updates/sec

Title: >US-08-817-547A-19
Description: (1-13) from US08817547A.pep
Perfect Score: 95
Sequence: 1 RKRLDPVHNFVAL 13

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 27.177; Variance 32.181; scale 0.844

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	95	100.0	115	1	PTHY_CANFA	8.93e-10
2	95	100.0	115	1	PTHY_BOVIN	8.93e-10
3	95	100.0	115	1	PTHY_PIG	8.93e-10
4	95	100.0	115	1	PTHY_HUMAN	8.93e-10
5	93	97.9	115	1	PTHY_RAT	3.05e-09
6	58	61.1	184	1	GLUC2_ARATH	8.46e-01
7	56	55.9	281	1	PZC1_YEAST	2.18e+00
8	56	58.9	444	1	CITR1_KLEPN	2.18e+00
9	56	58.9	475	1	STROMELYSIN-1	2.18e+00
10	56	58.9	477	1	COG3_MOUSE	2.18e+00
11	56	58.9	478	1	STROMELYSIN-1	2.18e+00
12	56	58.9	651	1	TOP3_HAEIN	2.18e+00
13	55	57.9	692	1	FSHR_RAT	3.46e+00
14	55	57.9	693	1	FSHR_CHICK	3.46e+00
15	54	56.8	102	1	YMH8_YEAST	5.46e+00
16	54	56.8	130	1	FILENSIN (LENS FIBER C	5.46e+00
17	54	56.8	525	1	Y107_METIA	5.46e+00
18	54	56.8	687	1	FSHR_EOVAR	5.46e+00
19	54	56.8	694	1	FSHR_HORSE	5.46e+00
20	54	56.8	752	1	HPRI_YEAST	5.46e+00
21	54	56.8	3444	1	POLG_PSVH	5.46e+00
22	53	55.8	462	1	COGM_MOUSE	8.55e+00
23	53	55.8	470	1	COGM_HUMAN	8.55e+00

24	53	55.8	471	1	HH_DROME	8.55e+00
25	53	55.8	609	1	LKHA_RAT	8.55e+00
26	53	55.8	610	1	LKHA_HUMAN	8.55e+00
27	53	55.8	610	1	LKHA_MOUSE	8.55e+00
28	53	55.8	632	1	Y242_MYCPN	8.55e+00
29	53	55.8	1321	1	MDR1_CABEL	8.55e+00
30	53	55.8	2133	1	FAB_PIG	8.55e+00
31	52	54.7	189	1	YNOO_YEAST	1.33e+01
32	52	54.7	476	1	COG3_RAT	1.33e+01
33	52	54.7	695	1	FSHR_BOVIN	1.33e+01
34	52	54.7	695	1	FSHR_SHEEP	1.33e+01
35	52	54.7	925	1	DEL_HUMAN	1.33e+01
36	51	53.7	119	1	RT13_ACAGA	2.06e+01
37	51	53.7	200	1	Y10P_ECOLI	2.06e+01
38	51	53.7	227	1	PRRA_RAT	2.06e+01
39	51	53.7	232	1	PM16_YEAST	2.06e+01
40	51	53.7	476	1	COG3_HUMAN	2.06e+01
41	51	53.7	636	1	RPOC_CYAPA	2.06e+01
42	51	53.7	695	1	FSHR_PIG	2.06e+01
43	51	53.7	1302	1	RRLP_BTV10	2.06e+01
44	51	53.7	1444	1	RRLP_RDV	2.06e+01
45	50	52.6	419	1	MYC1_XENLA	3.16e+01

ALIGNMENTS

RESULT	1	STANDARD;	PRT;	115 AA.
ID	PTHY_CANFA			
AC	P52212;			
DT	01-OCT-1996 (REL. 34, CREATED)			
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).			
GN	PTH.			
OS	CANIS FAMILIARIS (DOG).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; CARNIVORA.			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-PARATHYROID.			
RX	MEDLINE: 95369696.			
RA	ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,			
RL	DEWILLE J.W., CAPEN C.C.;			
CC	GENE 160:241-243(1995).			
CC	-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN			
CC	BONE AND PREVENTING THEIR RENAL EXCRETION.			
DR	EMBL: U15662; G558916; -			
DR	PROSITE: PS00335; PARATHYROID; 1.			
KW	HORMONE; SIGNAL.			
FT	SIGNAL	25	BY SIMILARITY.	
FT	PROPEP	26	31	PARATHYROID HORMONE.
FT	CHAIN	32	115	
SO	SEQUENCE	115 AA;	12957 MW;	16DEDEC CRC32;

Query Match 100.0%; Score 95; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 8.93e-10;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	56	RKRLDPVHNFVAL	68
Qy	1	RKRLDPVHNFVAL	13

RESULT 2
ID PTHY_BOVIN STANDARD; PRT; 115 AA.
AC P01268;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.
OS BOS TAPRUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

Search completed: Thu Jul 30 10:39:40 1998
Job time : 6 secs.

```

OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 80056617.
RA KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
RL POTS J.T., JR., RICH A.;
RL PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 82037785.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83105964.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL MOL. CELL. ENDOCRINOL. 28:411-424(1982).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84262483.
RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
RL GENE 28:319-329(1984).
RN [5]
RP SEQUENCE OF 26-115.
RX MEDLINE; 74142666.
RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T., JR.,
RL COHN D.V.;
RL PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
RN [6]
RP SEQUENCE OF 32-115.
RX MEDLINE; 71076162.
RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAMSON B.F.,
RL AUBACH G.D., POTTS J.T., JR.;
RL HOPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970).
RN [7]
RP SEQUENCE OF 32-115.
RX MEDLINE; 71063634.
RA BREWER H.B., JR., RONAN R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE; 71091588.
RA POTTS J.T., JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
RL DEFOS L.J., DAMSON B.F., HOGAN M.L., AUBACH G.D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL; V00106; G85; -.
DR EMBL; J00023; G163641; -.
DR EMBL; J00024; G163643; -.
DR EMBL; J00024; E18249; ALT_SEQ.
DR EMBL; J00024; E18250; ALT_INIT.
DR EMBL; K01938; G163647; -.
DR EMBL; M25082; G163645; -.
DR PIR: A01534; PTBO.
DR PIR: A24949; A24949.
DR PROSITE; PS00335; PARATHYROID; 1.
DR KW HORMONE; SIGNAL.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 PARATHYROID HORMONE.
FT CONFLICT 106 106 V -> G (IN REF. 4).
SQ SEQUENCE 115 AA; 12980 MW; 673EA5F2 CRC32;

Query Match 100.0%; Score 95; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 8,93e-10;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 56 RKKLDVHNHVAL 68
QY 1 RKKLDVHNHVAL 13

```


Query Match 64.2%; Score 61; DB 11; Length 207;
Best Local Similarity 66.7%; Pred. No. 2.58e-01;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Db 144 RLOEVHDFV 152
QY 3 KLDVHNFFV 11

Search completed: Thu Jul 30 10:40:55 1998
Job time : 57 secs.

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(TW)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:44:34 1998; MasPar time 2.69 Seconds
68.390 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-20
Description: (1-12) from US08817547A.pep
Perfect Score: 86
Sequence: 1 KKLQDVHNFVAL 12

Scoring table: PAM 150
Gap 15

Searched: 124785 segs, 15338987 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 18.088; Variance 63.020; scale 0.287

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	86	100.0	38	9	R58024 [Ala1,Ile2]-hPTH(1-38	6.03e-02
2	86	100.0	44	26	P30015 Human parathyroid hor	6.03e-02
3	86	100.0	47	25	W21946 Fusion protein compri	6.03e-02
4	86	100.0	84	27	W25687 Human parathyroid hor	6.03e-02
5	86	100.0	84	4	R23542 Bovine parathyroid ho	6.03e-02
6	86	100.0	84	4	R23471 Porcine parathyroid h	6.03e-02
7	86	100.0	84	4	R23387 Porcine parathyroid h	6.03e-02
8	86	100.0	84	4	R23262 Bovine parathyroid ho	6.03e-02
9	86	100.0	84	4	R23316 Bovine parathyroid ho	6.03e-02
10	86	100.0	84	4	R23346 Bovine parathyroid ho	6.03e-02
11	86	100.0	84	4	R23336 Bovine parathyroid ho	6.03e-02
12	86	100.0	84	4	R23429 Porcine parathyroid h	6.03e-02
13	86	100.0	84	4	R23259 Bovine parathyroid ho	6.03e-02
14	86	100.0	84	4	R23436 Porcine parathyroid h	6.03e-02
15	86	100.0	84	4	R23512 Bovine parathyroid hor	6.03e-02
16	86	100.0	84	4	R21157 Human parathyroid hor	6.03e-02
17	86	100.0	84	4	R21156 Human parathyroid hor	6.03e-02
18	86	100.0	84	4	R21185 Human parathyroid hor	6.03e-02
19	86	100.0	84	4	R21184 Human parathyroid hor	6.03e-02

20	86	100.0	84	4	R23371 Bovine parathyroid ho	6.03e-02
21	86	100.0	84	4	R23370 Bovine parathyroid ho	6.03e-02
22	86	100.0	84	25	W29420 Human parathyroid hor	6.03e-02
23	86	100.0	84	4	R21169 Human parathyroid hor	6.03e-02
24	86	100.0	84	4	R21170 Human parathyroid hor	6.03e-02
25	86	100.0	84	4	R21230 Human parathyroid hor	6.03e-02
26	86	100.0	84	4	R21231 Human parathyroid hor	6.03e-02
27	86	100.0	84	4	R21231 Human parathyroid hor	6.03e-02
28	86	100.0	84	4	R21212 Human parathyroid hor	6.03e-02
29	86	100.0	84	4	R23395 Porcine parathyroid ho	6.03e-02
30	86	100.0	84	4	R23283 Bovine parathyroid ho	6.03e-02
31	86	100.0	84	4	R21188 Human parathyroid hor	6.03e-02
32	86	100.0	84	4	R21189 Human parathyroid hor	6.03e-02
33	86	100.0	84	4	R21165 Human parathyroid hor	6.03e-02
34	86	100.0	84	4	R21164 Human parathyroid hor	6.03e-02
35	86	100.0	84	4	R23258 Bovine parathyroid ho	6.03e-02
36	86	100.0	84	4	R21168 Human parathyroid ho	6.03e-02
37	86	100.0	84	4	R23290 Bovine parathyroid ho	6.03e-02
38	86	100.0	84	4	R23402 Porcine parathyroid h	6.03e-02
39	86	100.0	84	4	R23275 Bovine parathyroid ho	6.03e-02
40	86	100.0	84	4	R23394 Porcine parathyroid h	6.03e-02
41	86	100.0	84	4	R21208 Human parathyroid hor	6.03e-02
42	86	100.0	84	4	R23904 Bovine parathyroid ho	6.03e-02
43	86	100.0	84	8	R42067 Human parathyroid hor	6.03e-02
44	86	100.0	84	8	R42067 Human parathyroid hor	6.03e-02
45	86	100.0	84	4	R23449 Porcine parathyroid h	6.03e-02

ALIGNMENTS

RESULT 1
ID R58024 standard; peptide; 38 AA.
AC R58024;
DT 20-SEP-1994 (first entry)
DE [Ala1,Ile2]-hPTH(1-38)-OH.
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
PN G8269176-A.
PD 02-FEB-1994.
PF 12-JUL-1993; 014384.
PR 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (BAUO) SANDOZ LTD.
PA (BAUO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F,
PI Gombert F, Gram H, Lewis I, Ramage F, Schneider H;
PI Waelchli R, Rainer A;
DR WPI: 94-018352/03.
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 10; Page 35; 92pp; English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 38 AA.
Query Match 100.0%; Score 86; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 6.03e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 26 kklqdvhnfval 37

QY 1 KKLQDVHNFVAL 12

RESULT

ID 2
 AC P30015 standard; peptide; 44 AA.
 DT 11-SEP-1992 (first entry)
 DE Human parathyroid hormone (1-44).
 KW HPH; condensation; azide; active ester; carbodilimide.
 OS Synthetic.
 PN J57192350-A.
 PD 26-NOV-1982.
 PE 22-APR-1981; JP-059750.
 PR (AJTN) TANPAKUSHITSU KENKY.
 DR WPI; 83-03106K/02 (03106K).
 PT Peptide fragment (1-44) of human parathyroid hormone - prepd. by
 PT removing protecting gps. from condensed peptide
 PT Claim 1, Page 1; 17pp; Japanese.
 CC The peptide fragment (1-44) can be prepd. by condensn. of individual
 CC amino acids or peptide fragments and removal of protecting groups
 CC from the condensed peptide in conventional manner. The peptide bond
 CC formation can be carried out pref. by azide method, active ester
 CC method or carbodilimide method. No use is given.
 SQ Sequence 44 AA;






Query Match

Best Local Similarity 100.0%; Score 86; DB 26; Length 44;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 26 kklqdvhnfval 37
 QY 1 KKLQDVHNFVAL 12

Search completed: Thu Jul 30 10:44:56 1998
 Job time : 22 secs.

(TM)

COMMENT Determination: NMR
 KEYWORDS disease mutation; hormone; signal
 FEATURE 2-9
 15-25 #region helix (right hand alpha)\
 SUMMARY #region helix (right hand alpha)
 #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 86; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 7.55e-06;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 23 KKLQDVHNFVAL 34
 |||||||||
 QY 1 KKLQDVHNFVAL 12

Search completed: Thu Jul 30 10:44:16 1998
 Job time : 27 secs.

MISSED

(TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:42:38 1998; MasPar time 2.23 Seconds
134.872 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-20
Description: (1-12) from US08817547A.pep
Perfect Score: 86
Sequence: 1 KKLQDVHNFVAL 12

Scoring table:
PAM 150
Gap 15

Searched: 69111 segs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 26.327; Variance 30.652; scale 0.859

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Query No.	Score	Match %	Length	ID	Description	Pred. No.
1	86	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	5.76e-08
2	86	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	5.76e-08
3	86	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	5.76e-08
4	86	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	5.76e-08
5	84	97.7	115	1	PTHY_RAT PARATHYROID HORMONE PR	1.95e-07
6	56	65.1	475	1	COG3_MOUSE STROMELYSIN-1 PRECURSOR	1.06e+00
7	56	65.1	478	1	COG3_RABIT STROMELYSIN-1 PRECURSOR	1.06e+00
8	56	65.1	651	1	TOP3_HAETN DNA TOPOISOMERASE III	1.06e+00
9	55	64.0	692	1	FSHR_RAT FOLLICLE STIMULATING H	1.72e+00
10	55	64.0	693	1	FSHR_CHICK FOLLICLE STIMULATING H	1.72e+00
11	54	62.8	525	1	Y107_METVA HYPOTHETICAL PROTEIN M	2.76e+00
12	54	62.8	687	1	FSHR_HORSE FOLLICLE STIMULATING H	2.76e+00
13	54	62.8	694	1	FSHR_HORSE FOLLICLE STIMULATING H	2.76e+00
14	54	62.8	3344	1	POLG_PRSVA GENOME POLYPROTEIN (CO	4.42e+00
15	53	61.6	471	1	HH_DROME HEDGEHOG PROTEIN PRECU	4.42e+00
16	53	61.6	609	1	LEUKOTRIENE A-4 HYDROL	4.42e+00
17	53	61.6	610	1	LKHA_HUMAN LEUKOTRIENE A-4 HYDROL	4.42e+00
18	53	61.6	610	1	LKHA_MOUSE LEUKOTRIENE A-4 HYDROL	4.42e+00
19	53	61.6	632	1	Y242_MYCPN HYPOTHETICAL PROTEIN M	4.42e+00
20	53	61.6	1321	1	MDRI_CAEEL MULTIDRUG RESISTANCE P	4.42e+00
21	52	60.5	476	1	COGX_RAT STROMELYSIN-2 PRECURSOR	7.01e+00
22	52	60.5	695	1	FSHR_BOVIN FOLLICLE STIMULATING H	7.01e+00

24	52	60.5	695	1	FSHR_SHEEP FOLLICLE STIMULATING H	7.01e+00
25	51	59.3	119	1	RT13_JACACA MITOCHONDRIAL RIBOSOMA	1.11e+01
26	51	59.3	200	1	Y1GP_ECOLI HYPOTHETICAL 22.3 KD P	1.11e+01
27	51	59.3	232	1	RM16_YEAST PROBABLE MITOCHONDRIAL	1.11e+01
28	51	59.3	476	1	COGX_HUMAN STROMELYSIN-2 PRECURSOR	1.11e+01
29	51	59.3	636	1	RPOC_CYAPA DNA-DIRECTED RNA POLYM	1.11e+01
30	51	59.3	695	1	FSHR_PIG FOLLICLE STIMULATING H	1.11e+01
31	51	59.3	925	1	DBL_HUMAN PROTO-ONCOGENE DBL PRE	1.11e+01
32	51	59.3	1444	1	RRPL_RDV RNA-DIRECTED RNA POLYM	1.11e+01
33	50	58.1	203	1	RPOC_PROHO DNA-DIRECTED RNA POLYM	1.73e+01
34	50	58.1	316	1	VSH5_DICDI VEGEATIVE SPECIFIC PR	1.73e+01
35	50	58.1	462	1	COGM_MOUSE MACROPHAGE METALLOELAS	1.73e+01
36	50	58.1	470	1	COGM_HUMAN MACROPHAGE METALLOELAS	1.73e+01
37	50	58.1	477	1	COG3_HUMAN STROMELYSIN-1 PRECURSOR	1.73e+01
38	50	58.1	543	1	VP61_NPVAC 61 KD PROTEIN.	1.73e+01
39	50	58.1	831	1	TVID_SALTI VI POLYACCHARIDE BIOS	1.73e+01
40	50	58.1	1177	1	MED_BACSV TRANSCRIPTION-REPAIR C	1.73e+01
41	50	58.1	1682	1	MSPI_PLAF3 MEROZOITE SURFACE PROT	1.73e+01
42	50	58.1	1701	1	MSPI_PLAF3 MEROZOITE SURFACE PROT	1.73e+01
43	50	58.1	1701	1	MSPI_PLAF3 MEROZOITE SURFACE PROT	1.73e+01
44	50	58.1	4349	1	DYHC_NECHA DYNEIN HEAVY CHAIN, CY	1.73e+01
45	49	57.0	908	1	ATMB_SALTY MG(2+) TRANSPORT ATPAS	2.69e+01

ALIGNMENTS

RESULT	ID	PTHY_CANFA	STANDARD	PRT	115 AA.
AC	P52212				
DT	01-OCT-1996	(REL. 34, CREATED)			
DT	01-OCT-1996	(REL. 34, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996	(REL. 34, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).				
GN	PTH.				
OS	CANIS FAMILIARIS (DOG).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUETHERIA; CARNIVORA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-PARATHYROID.				
RX	MEDLINE: 95369696.				
RA	ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,				
RL	GENE 160:241-243(1993).				
CC	-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN				
CC	BONE AND PREVENTING THEIR RENAL EXCRETION.				
DR	EMBL: U15662; G558916; "				
DR	PROSITE: PS00335; PARATHYROID; 1.				
KW	HORMONE; SIGNAL.				
FT	SIGNAL.				
FT	PROPEP				
FT	CHAIN				
SQ	SEQUENCE				
Query Match					
Best Local Similarity	100.0%;				
Matches	12; Conservative				
Db	57 KKLQDVHNFVAL 68				
Qy	1 KKLQDVHNFVAL 12				
RESULT	2				
ID	PTHY_BOVIN	STANDARD;	PRT;	115 AA.	
AC	P01268				
DT	21-JUL-1986	(REL. 01, CREATED)			
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).				
GN	PTH.				
OS	BOS TAURUS (BOVINE).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				

US-08-817-547A-20.rsp

Search completed: Thu Jul 30 10:42:44 1998
Job time : 6 secs.

OC EUTHERIA; ARTIODACTYLA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 80056617.
 RA KROMENBERG H.M., MCDEVITT B.E., NAJTOUB J.A., NATHANS J., SHARP P.
 RL POTS J.T. JR., RICH A.J.
 RN PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 82037785.
 RA WEAVER C.A., GORDON D.F., KEMPER B.;
 RL MOL. CELL. ENDOCRINOL. 28:411-424(1982).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 84282483.
 RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
 RL GENE 28:319-329(1984).
 RN [5]
 RP SEQUENCE OF 26-115.
 RX MEDLINE; 74142666.
 RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTS J.T. JR.
 RL PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
 RN [6]
 RP SEQUENCE OF 32-115.
 RX MEDLINE; 71076162.
 RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,
 RL AURBACH G.D., POTS J.T. JR.;
 RN HOPE-SEYLER S.Z. PHISTOL. CHEM. 351:1586-1588(1970).
 RP [7]
 RX SEQUENCE OF 32-115.
 RA BREMER H.B. JR., RONAN R.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
 RN [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE; 71091588.
 RA POTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
 RL DEFTOS J.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;
 RN PROC. NATL. ACAD. SCI. U.S.A. 66:65-67(1971).
 RP -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 BONE AND PREVENTING THEIR RENAL EXCRETION.
 RX EMBL; J00106; G85;
 RA EMBL; J00023; G163641;
 RL EMBL; J00024; G163643;
 RN EMBL; J00024; G18349; ALT_SEQ.
 RA EMBL; J00024; G18350; ALT_SEQ.
 RL EMBL; K01938; G16364; ALT_SEQ.
 RN EMBL; M25082; G16364; ALT_SEQ.
 RA PIR; A01534; PTBO.
 RL PIR; A24940; A24949.
 RN PROSITE; P500335; PARATHYROID; 1.
 KW HORMONE; SIGNAL.
 FT SIGNAL.
 FT PROPEP 1 25
 FT CHAIN 26 31
 FT CONFLICT 32 115
 SQ SEQUENCE 106 106
 V -> G (IN REF. 4).
 PARATHYROID HORMONE.
 673EAF2 CRC32.
 Query Match 100.0%; Score 86; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 5.76e-08;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
 Db 57 KILLDYNPAL 68
 1 KILLDYNPAL 12

Query Match 70.9%; Score 61; DB 11; Length 207;
Best Local Similarity 66.7%; Pred. No. 1.70e-01;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Db 144 RLOEVHDFV 152
QY 2 KLODVHNFV 10

Search completed: Thu Jul 30 10:43:30 1998
job time : 29 secs.

NWSENF
***** (TW)

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Mparch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:47:12 1998; MasPar time 2.77 Seconds
60.925 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-21
Description: (1-11) from US08817547A.pep
Perfect Score: 79
Sequence: 1 KLQDVHNEVAL 11

Scoring table: PAM 150
Gap 15

Searched: 124785 segs, 15338987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 17.545; Variance 61.494; scale 0.285
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	79	100.0	37	2	R1882 Parathyroid hormone f	2.64e-01
2	79	100.0	38	9	R58024 [Ala1, Ile2]-hPTH(1-38	2.64e-01
3	79	100.0	38	9	R58022 [Ile1]-hPTH(1-38)-OH	2.64e-01
4	79	100.0	38	9	R58123 [Ser19]-hPTH(1-38)-OH	2.64e-01
5	79	100.0	38	9	R58124 [Lys19]-hPTH(1-38)-OH	2.64e-01
6	79	100.0	38	9	R58149 [Ile22]-hPTH(1-38)-OH	2.64e-01
7	79	100.0	38	9	R58152 [Arg22]-hPTH(1-38)-OH	2.64e-01
8	79	100.0	38	9	R58153 [Arg26]-hPTH(1-38)-OH	2.64e-01
9	79	100.0	38	9	R58120 [Ala17]-hPTH(1-38)-OH	2.64e-01
10	79	100.0	38	9	R58119 [Gly16]-hPTH(1-38)-OH	2.64e-01
11	79	100.0	44	26	P30015 Human parathyroid hor	2.64e-01
12	79	100.0	47	25	W21945 Fusion protein compri	2.64e-01
13	79	100.0	84	27	W25687 Human parathyroid hor	2.64e-01
14	79	100.0	84	4	R23542 Bovine parathyroid h	2.64e-01
15	79	100.0	84	4	R23471 Porcine parathyroid h	2.64e-01
16	79	100.0	84	4	R23448 Porcine parathyroid h	2.64e-01
17	79	100.0	84	4	R23322 Bovine parathyroid ho	2.64e-01
18	79	100.0	84	4	R23345 Bovine parathyroid ho	2.64e-01
19	79	100.0	84	4	R23336 Bovine parathyroid ho	2.64e-01

ID	Score	Query Match	Length	DB ID	Description	Pred. No.
20	79	100.0	84	4	R23429 Porcine parathyroid h	2.64e-01
21	79	100.0	84	4	R23259 Bovine parathyroid ho	2.64e-01
22	79	100.0	84	4	R23485 Porcine parathyroid h	2.64e-01
23	79	100.0	84	4	R21257 Human parathyroid hor	2.64e-01
24	79	100.0	84	4	R21156 Human parathyroid hor	2.64e-01
25	79	100.0	84	4	R23483 Porcine parathyroid h	2.64e-01
26	79	100.0	84	25	W29420 Human parathyroid hor	2.64e-01
27	79	100.0	84	4	R23549 Bovine parathyroid ho	2.64e-01
28	79	100.0	84	4	R23327 Bovine parathyroid hor	2.64e-01
29	79	100.0	84	4	R21213 Human parathyroid hor	2.64e-01
30	79	100.0	84	4	R21212 Human parathyroid hor	2.64e-01
31	79	100.0	84	4	R21238 Human parathyroid hor	2.64e-01
32	79	100.0	84	4	R21183 Human parathyroid hor	2.64e-01
33	79	100.0	84	4	R21188 Human parathyroid hor	2.64e-01
34	79	100.0	84	4	R21189 Human parathyroid hor	2.64e-01
35	79	100.0	84	4	R23258 Bovine parathyroid hor	2.64e-01
36	79	100.0	84	4	R21168 Human parathyroid hor	2.64e-01
37	79	100.0	84	4	R23425 Porcine parathyroid h	2.64e-01
38	79	100.0	84	4	R21241 Human parathyroid hor	2.64e-01
39	79	100.0	84	4	R21170 Human parathyroid hor	2.64e-01
40	79	100.0	84	4	R21169 Human parathyroid hor	2.64e-01
41	79	100.0	84	8	R42068 Stability-enhanced hu	2.64e-01
42	79	100.0	84	8	R42074 Stability-enhanced hu	2.64e-01
43	79	100.0	84	4	R23449 Porcine parathyroid h	2.64e-01
44	79	100.0	114	4	P80306 Sequence of bovine pa	2.64e-01
45	79	100.0	115	4	P40251 Protein sequence incl	2.64e-01

ALIGNMENTS

RESULT 1
ID R1882 standard; protein; 37 AA.
AC R1882;
DT 24-JUL-1991 (first entry)
DE Parathyroid hormone fragment (1-37).
KW Parathyroid hormone; osteoporosis; hypertension; hypoparathyroidism;
KW kidney failure; hypertension; acute renal insufficiency.
OS Homo sapiens.
PN DE3935738-A.
PD 08-MAY-1991.
PF 27-OCT-1989; 935738.
PR 27-OCT-1989; DE:935738.
PA (FORS.) FORSMANN W.
PI Forsmann W-G, Herbst F, Schulz-Knappe P, Adermann K, Gagele M;
DR WPI; 91-141042/20.
PT New parathyroid hormone fragment and its naturally occurring
PT derivs. - used to treat osteoporosis, hypertension,
PT hypoparathyroidism, electrolyte imbalance associated with kidney
PT failure, etc.
PS Claim 1; page 6; 22pp; German.
CC This parathyroid hormone fragment, comprising residues 1-37, and its
CC derivs. are useful for treating parathyroid gland disorders,
CC degenerative bone disease, circulatory disease, lung disease, etc.
CC Antibodies raised against the fragment are useful for diagnosing
CC these diseases. The fragment and derivs. are administered as a
CC lyophilisate with mannitol.
SQ Sequence 37 AA:
Query Match 100.0%; Score 79; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.64e-01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 27 klqdvhnfval 37
QY 1 KLQDVHNEVAL 11
RESULT 2
ID R58024 standard; peptide; 38 AA.
AC R58024;
DT 20-SEP-1994 (first entry)
DE [Ala1, Ile2]-hPTH(1-38)-OH.
KW Human parathyroid hormone; hPTH; variant; analogue;

KM calcium: depletion; fixation; resorption; osteopathy; osteoporosis;
 KM hypoparathyroidism.
 OS Synthetic.
 PN GB269176-A.
 PD 02-FEB-1994.
 PF 12-JUL-1993; 014384.
 PR 15-JUL-1992; GB-015009.
 PR 18-DEC-1992; GB-026415.
 PR 23-DEC-1992; GB-026859.
 PR 23-DEC-1992; GB-026861.
 PR 28-JAN-1993; GB-001691.
 PR 28-JAN-1993; GB-001692.
 PR 14-APR-1993; GB-007673.
 PR 19-APR-1993; GB-008033.
 PA (SANO) SANDOZ LTD.
 PA (BAUE/) BAUER W.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F,
 Gombert F, Gram H, Lewis I, Ramage P, Schneider H,
 Waelchli R, Ralner A;
 WPI: 94-018352/03.
 PT New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc.
 PS Example 10; Page 35; 92pp; English.
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 SQ Sequence 38 AA;

Query Match 100.0%; Score 79; DB 9; Length 38;
 Best Local Similarity 100.0%; Pred. No. 2,64e-01;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 27 Klgdvhmfval 37
 |||||||||
 Oy 1 KLDVHNFVAL 11

Search completed: Thu Jul 30 10:47:36 1998
 Job time : 24 secs.

M P S R C H
(TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:46:26 1998; Maspar time 3.26 Seconds
Tabular output not generated. 123.145 Million cell updates/sec

Title: >US-08-817-547A-21
Description: (1-11) from US08817547A.pep
Perfect Score: 79
Sequence: 1 KLQDVHNFVAL 11

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr56
1:plr1 2:plr2 3:plr3 4:plr4 5:nrl3d

Statistics: Mean 24.418; Variance 35.126; scale 0.695

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	79	100.0	34	5 12WE	parathyroid hormone (7.53e-05	
2	79	100.0	34	5 12WG	parathyroid hormone (7.53e-05	
3	79	100.0	34	5 12WF	parathyroid hormone 4 7.53e-05	
4	79	100.0	35	5 12WD	parathyroid hormone (7.53e-05	
5	79	100.0	36	5 12WB	parathyroid hormone (7.53e-05	
6	79	100.0	37	5 12WH	parathyroid hormone (7.53e-05	
7	79	100.0	37	5 12WC	parathyroid hormone (7.53e-05	
8	79	100.0	115	1 PJRU	parathyroid hormone (7.53e-05	
9	79	100.0	115	1 JCA202	parathyroid hormone (7.53e-05	
10	79	100.0	115	1 PTPG	parathyroid hormone (7.53e-05	
11	79	100.0	115	1 PTEB	parathyroid hormone (7.53e-05	
12	77	97.5	115	1 A05091	parathyroid hormone p 2.03e-02	
13	67	84.8	105	2 I51851	parathyroid hormone - 2.48e-01	
14	60	75.9	34	5 12WH	cyclic parathyroid ho 5.75e-01	
15	60	75.9	34	5 12WA	parathyroid hormone (1.11e+01	
16	53	67.1	555	2 S69641	hypothetical protein (1.11e+01	
17	53	67.1	632	2 S73824	M6242 homolog H91_orf 1.11e+01	
18	53	67.1	1321	2 S27337	multidrug resistance 1.11e+01	
19	52	65.8	606	2 S13526	hydrogenase homolog, 1.66e+01	
20	51	64.6	201	2 C65188	hypothetical 22.3 kd 2.48e+01	
21	51	64.6	232	2 S50292	ribosomal protein L16 2.48e+01	
22	51	64.6	1444	1 A43377	RNA-directed RNA poly 2.48e+01	
23	50	63.3	217	2 E70126	hypothetical protein 3.67e+01	

24	50	63.3	462	2	A42401	macrophage elastase (3.67e+01
25 <td>50<td>63.3<td>470<td>2<td>A49499<td>metalloelastase HME (3.67e+01</td></td></td></td></td></td>	50 <td>63.3<td>470<td>2<td>A49499<td>metalloelastase HME (3.67e+01</td></td></td></td></td>	63.3 <td>470<td>2<td>A49499<td>metalloelastase HME (3.67e+01</td></td></td></td>	470 <td>2<td>A49499<td>metalloelastase HME (3.67e+01</td></td></td>	2 <td>A49499<td>metalloelastase HME (3.67e+01</td></td>	A49499 <td>metalloelastase HME (3.67e+01</td>	metalloelastase HME (3.67e+01
26 <td>50<td>63.3<td>543<td>2<td>H40781<td>hypothetical 60.7k pr 3.67e+01</td></td></td></td></td></td>	50 <td>63.3<td>543<td>2<td>H40781<td>hypothetical 60.7k pr 3.67e+01</td></td></td></td></td>	63.3 <td>543<td>2<td>H40781<td>hypothetical 60.7k pr 3.67e+01</td></td></td></td>	543 <td>2<td>H40781<td>hypothetical 60.7k pr 3.67e+01</td></td></td>	2 <td>H40781<td>hypothetical 60.7k pr 3.67e+01</td></td>	H40781 <td>hypothetical 60.7k pr 3.67e+01</td>	hypothetical 60.7k pr 3.67e+01
27 <td>50<td>63.3<td>543<td>2<td>S25128<td>61k protein - Autogra 3.67e+01</td></td></td></td></td></td>	50 <td>63.3<td>543<td>2<td>S25128<td>61k protein - Autogra 3.67e+01</td></td></td></td></td>	63.3 <td>543<td>2<td>S25128<td>61k protein - Autogra 3.67e+01</td></td></td></td>	543 <td>2<td>S25128<td>61k protein - Autogra 3.67e+01</td></td></td>	2 <td>S25128<td>61k protein - Autogra 3.67e+01</td></td>	S25128 <td>61k protein - Autogra 3.67e+01</td>	61k protein - Autogra 3.67e+01
28 <td>50<td>63.3<td>653<td>2<td>S40449<td>pro-hormone convertas 3.67e+01</td></td></td></td></td></td>	50 <td>63.3<td>653<td>2<td>S40449<td>pro-hormone convertas 3.67e+01</td></td></td></td></td>	63.3 <td>653<td>2<td>S40449<td>pro-hormone convertas 3.67e+01</td></td></td></td>	653 <td>2<td>S40449<td>pro-hormone convertas 3.67e+01</td></td></td>	2 <td>S40449<td>pro-hormone convertas 3.67e+01</td></td>	S40449 <td>pro-hormone convertas 3.67e+01</td>	pro-hormone convertas 3.67e+01
29 <td>50<td>63.3<td>731<td>2<td>S28491<td>hypothetical protein 3.67e+01</td></td></td></td></td></td>	50 <td>63.3<td>731<td>2<td>S28491<td>hypothetical protein 3.67e+01</td></td></td></td></td>	63.3 <td>731<td>2<td>S28491<td>hypothetical protein 3.67e+01</td></td></td></td>	731 <td>2<td>S28491<td>hypothetical protein 3.67e+01</td></td></td>	2 <td>S28491<td>hypothetical protein 3.67e+01</td></td>	S28491 <td>hypothetical protein 3.67e+01</td>	hypothetical protein 3.67e+01
30 <td>50<td>63.3<td>831<td>2<td>D36892<td>V1PC 5'-region hypoch 3.67e+01</td></td></td></td></td></td>	50 <td>63.3<td>831<td>2<td>D36892<td>V1PC 5'-region hypoch 3.67e+01</td></td></td></td></td>	63.3 <td>831<td>2<td>D36892<td>V1PC 5'-region hypoch 3.67e+01</td></td></td></td>	831 <td>2<td>D36892<td>V1PC 5'-region hypoch 3.67e+01</td></td></td>	2 <td>D36892<td>V1PC 5'-region hypoch 3.67e+01</td></td>	D36892 <td>V1PC 5'-region hypoch 3.67e+01</td>	V1PC 5'-region hypoch 3.67e+01
31 <td>50<td>63.3<td>1323<td>2<td>PN0568<td>connectin 3B - chickc 5.40e+01</td></td></td></td></td></td>	50 <td>63.3<td>1323<td>2<td>PN0568<td>connectin 3B - chickc 5.40e+01</td></td></td></td></td>	63.3 <td>1323<td>2<td>PN0568<td>connectin 3B - chickc 5.40e+01</td></td></td></td>	1323 <td>2<td>PN0568<td>connectin 3B - chickc 5.40e+01</td></td></td>	2 <td>PN0568<td>connectin 3B - chickc 5.40e+01</td></td>	PN0568 <td>connectin 3B - chickc 5.40e+01</td>	connectin 3B - chickc 5.40e+01
32 <td>49<td>62.0<td>142<td>2<td>B40535<td>clathrin-associated p 5.40e+01</td></td></td></td></td></td>	49 <td>62.0<td>142<td>2<td>B40535<td>clathrin-associated p 5.40e+01</td></td></td></td></td>	62.0 <td>142<td>2<td>B40535<td>clathrin-associated p 5.40e+01</td></td></td></td>	142 <td>2<td>B40535<td>clathrin-associated p 5.40e+01</td></td></td>	2 <td>B40535<td>clathrin-associated p 5.40e+01</td></td>	B40535 <td>clathrin-associated p 5.40e+01</td>	clathrin-associated p 5.40e+01
33 <td>49<td>62.0<td>145<td>5<td>1AT0</td><td>17-hedgehog 17-kda fir 5.40e+01</td></td></td></td></td>	49 <td>62.0<td>145<td>5<td>1AT0</td><td>17-hedgehog 17-kda fir 5.40e+01</td></td></td></td>	62.0 <td>145<td>5<td>1AT0</td><td>17-hedgehog 17-kda fir 5.40e+01</td></td></td>	145 <td>5<td>1AT0</td><td>17-hedgehog 17-kda fir 5.40e+01</td></td>	5 <td>1AT0</td> <td>17-hedgehog 17-kda fir 5.40e+01</td>	1AT0	17-hedgehog 17-kda fir 5.40e+01
34 <td>49<td>62.0<td>316<td>2<td>S07569</td><td>protein H5 - slime mo 5.40e+01</td></td></td></td></td>	49 <td>62.0<td>316<td>2<td>S07569</td><td>protein H5 - slime mo 5.40e+01</td></td></td></td>	62.0 <td>316<td>2<td>S07569</td><td>protein H5 - slime mo 5.40e+01</td></td></td>	316 <td>2<td>S07569</td><td>protein H5 - slime mo 5.40e+01</td></td>	2 <td>S07569</td> <td>protein H5 - slime mo 5.40e+01</td>	S07569	protein H5 - slime mo 5.40e+01
35 <td>49<td>62.0<td>455<td>2<td>A26081<td>epoxide hydrolase (EC 5.40e+01</td></td></td></td></td></td>	49 <td>62.0<td>455<td>2<td>A26081<td>epoxide hydrolase (EC 5.40e+01</td></td></td></td></td>	62.0 <td>455<td>2<td>A26081<td>epoxide hydrolase (EC 5.40e+01</td></td></td></td>	455 <td>2<td>A26081<td>epoxide hydrolase (EC 5.40e+01</td></td></td>	2 <td>A26081<td>epoxide hydrolase (EC 5.40e+01</td></td>	A26081 <td>epoxide hydrolase (EC 5.40e+01</td>	epoxide hydrolase (EC 5.40e+01
36 <td>49<td>62.0<td>471<td>2<td>A46400<td>segment polarity prot 5.40e+01</td></td></td></td></td></td>	49 <td>62.0<td>471<td>2<td>A46400<td>segment polarity prot 5.40e+01</td></td></td></td></td>	62.0 <td>471<td>2<td>A46400<td>segment polarity prot 5.40e+01</td></td></td></td>	471 <td>2<td>A46400<td>segment polarity prot 5.40e+01</td></td></td>	2 <td>A46400<td>segment polarity prot 5.40e+01</td></td>	A46400 <td>segment polarity prot 5.40e+01</td>	segment polarity prot 5.40e+01
37 <td>49<td>62.0<td>471<td>3<td>A43480<td>segmentation gene hed 5.40e+01</td></td></td></td></td></td>	49 <td>62.0<td>471<td>3<td>A43480<td>segmentation gene hed 5.40e+01</td></td></td></td></td>	62.0 <td>471<td>3<td>A43480<td>segmentation gene hed 5.40e+01</td></td></td></td>	471 <td>3<td>A43480<td>segmentation gene hed 5.40e+01</td></td></td>	3 <td>A43480<td>segmentation gene hed 5.40e+01</td></td>	A43480 <td>segmentation gene hed 5.40e+01</td>	segmentation gene hed 5.40e+01
38 <td>49<td>62.0<td>475<td>1<td>KCRTH</td><td>stromelysin 1 (EC 3.4 5.40e+01</td></td></td></td></td>	49 <td>62.0<td>475<td>1<td>KCRTH</td><td>stromelysin 1 (EC 3.4 5.40e+01</td></td></td></td>	62.0 <td>475<td>1<td>KCRTH</td><td>stromelysin 1 (EC 3.4 5.40e+01</td></td></td>	475 <td>1<td>KCRTH</td><td>stromelysin 1 (EC 3.4 5.40e+01</td></td>	1 <td>KCRTH</td> <td>stromelysin 1 (EC 3.4 5.40e+01</td>	KCRTH	stromelysin 1 (EC 3.4 5.40e+01
39 <td>49<td>62.0<td>477<td>1<td>KCMSI</td><td>stromelysin 1 (EC 3.4 5.40e+01</td></td></td></td></td>	49 <td>62.0<td>477<td>1<td>KCMSI</td><td>stromelysin 1 (EC 3.4 5.40e+01</td></td></td></td>	62.0 <td>477<td>1<td>KCMSI</td><td>stromelysin 1 (EC 3.4 5.40e+01</td></td></td>	477 <td>1<td>KCMSI</td><td>stromelysin 1 (EC 3.4 5.40e+01</td></td>	1 <td>KCMSI</td> <td>stromelysin 1 (EC 3.4 5.40e+01</td>	KCMSI	stromelysin 1 (EC 3.4 5.40e+01
40 <td>49<td>62.0<td>478<td>1<td>KCRBS1</td><td>stromelysin 1 (EC 3.4 5.40e+01</td></td></td></td></td>	49 <td>62.0<td>478<td>1<td>KCRBS1</td><td>stromelysin 1 (EC 3.4 5.40e+01</td></td></td></td>	62.0 <td>478<td>1<td>KCRBS1</td><td>stromelysin 1 (EC 3.4 5.40e+01</td></td></td>	478 <td>1<td>KCRBS1</td><td>stromelysin 1 (EC 3.4 5.40e+01</td></td>	1 <td>KCRBS1</td> <td>stromelysin 1 (EC 3.4 5.40e+01</td>	KCRBS1	stromelysin 1 (EC 3.4 5.40e+01
41 <td>49<td>62.0<td>651<td>2<td>G64068<td>DNA topoisomerase (EC 5.40e+01</td></td></td></td></td></td>	49 <td>62.0<td>651<td>2<td>G64068<td>DNA topoisomerase (EC 5.40e+01</td></td></td></td></td>	62.0 <td>651<td>2<td>G64068<td>DNA topoisomerase (EC 5.40e+01</td></td></td></td>	651 <td>2<td>G64068<td>DNA topoisomerase (EC 5.40e+01</td></td></td>	2 <td>G64068<td>DNA topoisomerase (EC 5.40e+01</td></td>	G64068 <td>DNA topoisomerase (EC 5.40e+01</td>	DNA topoisomerase (EC 5.40e+01
42 <td>49<td>62.0<td>779<td>2<td>S50054<td>chloride channel prot 5.40e+01</td></td></td></td></td></td>	49 <td>62.0<td>779<td>2<td>S50054<td>chloride channel prot 5.40e+01</td></td></td></td></td>	62.0 <td>779<td>2<td>S50054<td>chloride channel prot 5.40e+01</td></td></td></td>	779 <td>2<td>S50054<td>chloride channel prot 5.40e+01</td></td></td>	2 <td>S50054<td>chloride channel prot 5.40e+01</td></td>	S50054 <td>chloride channel prot 5.40e+01</td>	chloride channel prot 5.40e+01
43 <td>49<td>62.0<td>1490<td>2<td>JC5145<td>DNA (cytosine-5'-) -met 5.40e+01</td></td></td></td></td></td>	49 <td>62.0<td>1490<td>2<td>JC5145<td>DNA (cytosine-5'-) -met 5.40e+01</td></td></td></td></td>	62.0 <td>1490<td>2<td>JC5145<td>DNA (cytosine-5'-) -met 5.40e+01</td></td></td></td>	1490 <td>2<td>JC5145<td>DNA (cytosine-5'-) -met 5.40e+01</td></td></td>	2 <td>JC5145<td>DNA (cytosine-5'-) -met 5.40e+01</td></td>	JC5145 <td>DNA (cytosine-5'-) -met 5.40e+01</td>	DNA (cytosine-5'-) -met 5.40e+01
44 <td>49<td>62.0<td>1495<td>2<td>S22610<td>DNA (cytosine-5'-) -met 5.40e+01</td></td></td></td></td></td>	49 <td>62.0<td>1495<td>2<td>S22610<td>DNA (cytosine-5'-) -met 5.40e+01</td></td></td></td></td>	62.0 <td>1495<td>2<td>S22610<td>DNA (cytosine-5'-) -met 5.40e+01</td></td></td></td>	1495 <td>2<td>S22610<td>DNA (cytosine-5'-) -met 5.40e+01</td></td></td>	2 <td>S22610<td>DNA (cytosine-5'-) -met 5.40e+01</td></td>	S22610 <td>DNA (cytosine-5'-) -met 5.40e+01</td>	DNA (cytosine-5'-) -met 5.40e+01
45 <td>49<td>62.0<td>1537<td>2<td>JC4172<td>DNA (cytosine-5'-) -met 5.40e+01</td></td></td></td></td></td>	49 <td>62.0<td>1537<td>2<td>JC4172<td>DNA (cytosine-5'-) -met 5.40e+01</td></td></td></td></td>	62.0 <td>1537<td>2<td>JC4172<td>DNA (cytosine-5'-) -met 5.40e+01</td></td></td></td>	1537 <td>2<td>JC4172<td>DNA (cytosine-5'-) -met 5.40e+01</td></td></td>	2 <td>JC4172<td>DNA (cytosine-5'-) -met 5.40e+01</td></td>	JC4172 <td>DNA (cytosine-5'-) -met 5.40e+01</td>	DNA (cytosine-5'-) -met 5.40e+01

ALIGNMENTS

RESULT	1	12WE	#type complete
ENTRY			parathyroid hormone (residues 4-37) - human
TITLE			HPTH(4-37)
ALTERNATE_NAMES			structure of human parathyroid hormone fragment 4-37, NMR 10
PDB_TITLE			structures
ORGANISM			#formal_name Homo sapiens #common_name man
REFERENCE			A67860
#authors			Roesch, P.; Marx, U.C.
#submission			submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references			PDB:12WE
REFERENCE			TN001721
#authors			Marx, U.C.
#book			In Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996
COMMENT			Resolution: not applicable
COMMENT			Determination: NMR
KEYWORDS			hormone
FEATURE			
15-25			
SUMMARY			#region helix (right hand alpha)
			length 34 #molecular-weight 4128 #checksum 5508
Query Match			100.0%; Score 79; DB 5; Length 34;
Best Local Similarity			100.0%; Pred. No. 7.53e-05;
Matches			11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	24	KLQDVHNFVAL 34	
Qy	1	KLQDVHNFVAL 11	
RESULT	2	12WG	#type complete
ENTRY			parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -
TITLE			synthetic
ALTERNATE_NAMES			n-succinyl-hPTH(4-37)
PDB_TITLE			succinyl human parathyroid hormone 4-37, NMR, 10 structures
ORGANISM			#formal_name synthetic
REFERENCE			A67743
#authors			Roesch, P.; Marx, U.C.
#submission			submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references			PDB:12WG
REFERENCE			TN003319
#authors			Marx, U.C.
#book			In Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996
COMMENT			Resolution: not applicable

```

COMMENT      Determination: NMR
KEYWORDS     disease mutation; hormone; signal
FEATURE      2-9
             15-25
SUMMARY      #region helix (right hand alpha)\
             #region helix (right hand alpha)
             #length 34 #molecular-weight 4128 #checksum 5508

Query Match  100.0%; Score 79; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.53e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 KLQDVHNFVAL 34
   |||||||||
QY 1 KLQDVHNFVAL 11

Search completed: Thu Jul 30 10:46:54 1998
Job time : 28 secs.

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 RELEASE (TM)

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MPsrch_dp protein - protein database search, using Smith-Waterman algorithm
 on: Thu Jul 30 10:45:13 1998; Maspar time 2.26 Seconds
 Tabular output not generated. 122.035 Million cell updates/sec

Title: >US-08-817-547A-21
 Description: (1-11) from US08817547A.pep
 Perfect Score: 79
 Sequence: 1 KLDVHNFVAL 11

Scoring table: PAM 150
 Gap 15

Searched: 69111 seqs. 25083644 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot35
 1:swiss1

Statistics: Mean 25.575; Variance 28.974; scale 0.883

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	79	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	1.01e-06
2	79	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	1.01e-06
3	79	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	1.01e-06
4	79	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	1.01e-06
5	77	97.5	115	1	PTHY_RAT PARATHYROID HORMONE PR	3.45e-06
6	53	67.1	1321	1	Y242_MYCN HYPOTHETICAL PROTEIN M	2.15e+00
7	53	67.1	1321	1	MDRI_CAEEL MULTIDRUG RESISTANCE P	5.64e+00
8	51	64.6	200	1	YIGP_ECOLI HYPOTHETICAL 22.3 KD P	5.64e+00
9	51	64.6	232	1	RM16_YEAST PROBABLE MITOCHONDRIAL	5.64e+00
10	51	64.6	1444	1	RRPL_RNV RNA-DIRECTED RNA POLYM	5.64e+00
11	50	63.3	462	1	COGM_MOUSE MACROPHAGE METALLOELAS	9.04e+00
12	50	63.3	470	1	COGM_MOUSE MACROPHAGE METALLOELAS	9.04e+00
13	50	63.3	543	1	VP61_NPVAC 61 KD PROTEIN.	9.04e+00
14	50	63.3	831	1	TYID_SALTI VI POLYSACCHARIDE BIOS	9.04e+00
15	49	62.0	142	1	AP17_RAT CLATHRIN COAT ASSEMBLY	1.44e+01
16	49	62.0	142	1	AP17_HUMAN CLATHRIN COAT ASSEMBLY	1.44e+01
17	49	62.0	316	1	VSH5_DICDI VEGTATIVE SPECIFIC PR	1.44e+01
18	49	62.0	455	1	HYEP_RAT EPOXIDE HYDROLASE (PC	1.44e+01
19	49	62.0	471	1	HH_DROME HEDGEHOG PROTEIN PRECU	1.44e+01
20	49	62.0	475	1	COG3_RAT STROMEYLSIN-1 PRECURSOR	1.44e+01
21	49	62.0	477	1	COG3_MOUSE STROMEYLSIN-1 PRECURSOR	1.44e+01
22	49	62.0	478	1	COG3_RABIT STROMEYLSIN-1 PRECURSOR	1.44e+01
23	49	62.0	651	1	TOP3_HAEIN DNA TOPOISOMERASE III	1.44e+01

RESULT	ID	PTHY_CANFA	STANDARD	PRT	115 AA.	ALIGNMENTS
AC	P52212					
DT	01-OCT-1996	(REL. 34, CREATED)				
DT	01-OCT-1996	(REL. 34, LAST SEQUENCE UPDATE)				
DT	01-OCT-1996	(REL. 34, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).					
GN	PTH.					
OS	CANIS FAMILIARIS (DOG).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
OC	ETHERIA; CARNIVORA.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE-PARATHYROID.					
RX	MEDLINE: 95369696.					
RA	ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,					
RL	DEWILDE J.W., CAPER C.C.;					
CC	GENE 160:241-243(1995).					
CC	-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN					
CC	BONE AND PREVENTING THEIR RENAL EXCRETION.					
DR	EMBL: U15662; G558916; -.					
DR	PROSITE: PS00335; PARATHYROID; 1.					
KW	HORMONE; SIGNAL.					
FT	SIGNAL	1	25			
FT	PROPEP	26	31			
FT	CHAIN	32	115			
SQ	SEQUENCE	115 AA; 12957 MW; 16ED0EBC CRC32;				
Query Match						
Best local Similarity 100.0%; Score 79; DB 1; Length 115;						
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Db	58 KLDVHNFVAL 68					
QY	1 KLDVHNFVAL 11					
RESULT 2						
ID	PTHY_BOVIN	STANDARD;	PRT;	115 AA.		
AC	P01268;					
DT	21-JUL-1986	(REL. 01, CREATED)				
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).					
GN	PTH.					
OS	BOS TAURUS (BOVINE).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					

Search completed: Thu Jul 30 10:45:20 1998
Job time : 7 secs.

OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 80056617.
RA KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
RA POTTS J.T. JR., RICH A.;
RA PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 82037785.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RA PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 83105964.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RA MOL. CELL. ENDOCRINOL. 28:411-424(1982).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE: 84262483.
RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
RA GENE 28:319-329(1984).
RN [5]
RP SEQUENCE OF 26-115.
RX MEDLINE: 74142666.
RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,
RA COHN D.V.;
RA PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
RN [6]
RP SEQUENCE OF 32-115.
RX MEDLINE: 71076162.
RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,
RA AURBACH G.D., POTTS J.T. JR.;
RA HOPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).
RN [7]
RP SEQUENCE OF 32-115.
RX MEDLINE: 71063634.
RA BREWER H.B. JR., RONAN R.;
RA PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE: 71091588.
RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
RA DEPOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;
RA PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
RN [9]
RP FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
RN BONE AND PREVENTING THEIR RENAL EXCRETION.
CC EMBL: V00106; 685; -;
DR EMBL: J00023; G163641; -;
DR EMBL: J00024; G163643; -;
DR EMBL: J00024; E18249; ALT_SEQ.
DR EMBL: J00024; E18250; ALT_INIT.
DR EMBL: K01938; G163647; -;
DR EMBL: M25082; G163645; -;
DR PIR: A01534; PTBO.
DR PIR: A24949; A24949.
DR PROSITE: PS00335; PARATHYROID; 1.
KM HORMONE; SIGNAL.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 PARATHYROID HORMONE.
FT CONFLICT 106 106 V -> G (IN REF. 4).
FT FT 106 106
SQ SEQUENCE 115 AA; 12980 MW; 673EA5F2 CRC32;

Query Match 100.0%; Score 79; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.01e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 58 KLDVHNFVAL 68
OY 1 KLDVHNFVAL 11

WILEY
(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:45:37 1998; MasPar time 3.84 Seconds
Tabular output not generated. 120.566 Million cell updates/sec

Title: >US-08-817-547A-21
Description: (1-11) from US08817547A.pep
Perfect Score: 79
Sequence: 1 KLQDVHNFVAL 11

Scoring table:
PAM 150
Gap 15

Searched: 140542 seqs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 24.328; Variance 30.213; scale 0.805
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	67	84.8	105	10	PARATHYROID HORMONE (F	3.43e-03
2	61	77.2	207	11	ORF36L.	7.88e-02
3	54	68.4	993	3	VINCULIN.	2.47e+00
4	53	67.1	342	11	SIMILAR TO BACTERIOPHA	3.95e+00
5	53	67.1	555	1	D8035.17P.	3.95e+00
6	53	67.1	1321	3	KOBE7.9.	3.95e+00
7	52	65.8	345	9	STRA.	6.28e+00
8	52	65.8	606	9	HYD GAMMA.	6.28e+00
9	51	64.6	232	1	URAT CTP SYNTHETASE.	9.94e+00
10	51	64.6	1283	3	SIMILAR TO MULTIDRUG-R	9.94e+00
11	51	64.6	1444	11	RNA-DEPENDENT RNA POLY	9.94e+00
12	50	63.3	207	4	ARYLALKYLAMINE N-ACETY	1.56e+01
13	50	63.3	360	9	HYDROGENASE SMALL SUBU	1.56e+01
14	50	63.3	402	12	FERROCHLATASE (EC 4.9	1.56e+01
15	50	63.3	463	10	MACROPHAGE METALLOELAS	1.56e+01
16	50	63.3	483	12	STROMELYSIN-1/2-A.	1.56e+01
17	50	63.3	653	3	PREPRO-HORMONE CONVERT	1.56e+01
18	50	63.3	653	3	NEUROENDOCRINE CONVERT	1.56e+01
19	50	63.3	660	3	PC2.	1.56e+01
20	50	63.3	761	3	SIMILAR TO THE ATP-BIN	1.56e+01

21	50	63.3	1254	3	026599	1.56e+01
22	50	63.3	1323	12	008476	1.56e+01
23	50	63.3	4162	12	098918	2.44e+01
24	49	62.0	142	3	019123	2.44e+01
25	49	62.0	227	4	028974	2.44e+01
26	49	62.0	227	4	028972	2.44e+01
27	49	62.0	227	4	028973	2.44e+01
28	49	62.0	299	3	019742	2.44e+01
29	49	62.0	455	10	P97869	2.44e+01
30	49	62.0	477	4	028397	2.44e+01
31	49	62.0	726	3	027936	2.44e+01
32	49	62.0	732	3	P91676	2.44e+01
33	49	62.0	743	3	017305	2.44e+01
34	49	62.0	1190	3	020187	2.44e+01
35	49	62.0	1490	12	P79922	2.44e+01
36	49	62.0	1537	12	092072	2.44e+01
37	49	62.0	1564	4	028689	2.44e+01
38	49	62.0	1774	3	093636	2.44e+01
39	49	62.0	1918	3	093637	2.44e+01
40	48	60.8	232	9	P95776	3.78e+01
41	48	60.8	377	3	017273	3.78e+01
42	48	60.8	453	1	004934	3.78e+01
43	48	60.8	693	12	090719	3.78e+01
44	48	60.8	787	9	032799	3.78e+01
45	48	60.8	1289	3	001495	3.78e+01

ALIGNMENTS

RESULT 1
ID 063473; PRELIMINARY; PRT; 105 AA.
AC 063473;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE (FRAGMENT).
GN PTH.
OS RATTUS NORVEGICUS (RAT).
OC EUARCHYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUMARHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-THYROID, AND PARATHYROID;
RA SCHMELZER H.J., GROSS G., MAYER H.;
RL ADV. GENE TECHNOL. 21:228-229(1984).
DR EMBL; M54875; G601933; -.
FT NON-TER 1
SQ SEQUENCE 105 AA; 11746 MM; 6AC3163E CRC32;

Query Match 84.8%; Score 67; DB 10; Length 105;
Best Local Similarity 81.8%; Pred. No. 3.43e-03;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 48 KLQDVHNFVAL 58
QY 1 KLQDVHNFVAL 11
[1]
RESULT 2
ID 039628; PRELIMINARY; PRT; 207 AA.
AC 039628;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE ORF36L.
OS CYCIA POMONELLA GRANULOVIRUS.
OC VIRUSES; DSDNA VIRUSES, NO RNA STAGE; BACULOVIRIDAE; GRANULOVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RA JEHLE J.A., VAN DER LINDEN I.F.A., VLAK J.M.;
RL VIRUS RES. 0:0-0(1997).
DR EMBL; AF002732; G2232189; -.
SQ SEQUENCE 207 AA; 23915 MM; D2F0E988 CRC32;

Query Match 77.2%; Score 61; DB 11; Length 207;
Best Local Similarity 66.7%; Pred. No. 7.88e-02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
DB 144 RLOEVHDFV 152
QY 1 KLDVHNEV 9

Search completed: Thu Jul 30 10:46:08 1998
Job time : 31 secs.

 W I S E N H (TM)

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Msearch_pp protein - protein database search, using Smith-Waterman algorithm
 on: Thu Jul 30 10:50:05 1998; MasPar time 2.64 Seconds
 58.155 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-817-547A-22
 Description: (1-10) from US08817547A.pep
 Perfect Score: 72
 Sequence: 1 LQDVHNFVAL 10

Scoring table:
 PAM 150
 Gap 15

Searched: 124785 seqs, 15338987 residues
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:
 a-geneseg31-2
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27

Statistics: Mean 16.979; Variance 58.346; scale 0.291
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	72	100.0	38	9 R58151	[Ser22]-hPTH(1-38)-OH	8.81e-01
2	72	100.0	38	9 R58153	[Arg26]-hPTH(1-38)-OH	8.81e-01
3	72	100.0	38	9 R58022	[Ile1]-hPTH(1-38)-OH	8.81e-01
4	72	100.0	38	9 R58140	[Phe21]-hPTH(1-38)-OH	8.81e-01
5	72	100.0	38	9 R58142	[Asn21]-hPTH(1-38)-OH	8.81e-01
6	72	100.0	38	9 R58129	[His19]-hPTH(1-38)-OH	8.81e-01
7	72	100.0	38	9 R58133	[Asp19]-hPTH(1-38)-OH	8.81e-01
8	72	100.0	44	26 P30015	Human parathyroid hor	8.81e-01
9	72	100.0	47	25 W21946	Fusion protein compri	8.81e-01
10	72	100.0	84	27 W25687	Human parathyroid hor	8.81e-01
11	72	100.0	84	4 R23237	Human parathyroid hor	8.81e-01
12	72	100.0	84	4 R23192	Human parathyroid hor	8.81e-01
13	72	100.0	84	4 R23309	Bovine parathyroid ho	8.81e-01
14	72	100.0	84	4 R23276	Bovine parathyroid ho	8.81e-01
15	72	100.0	84	4 R21254	Human parathyroid hor	8.81e-01
16	72	100.0	84	4 R23429	Porcine parathyroid h	8.81e-01
17	72	100.0	84	4 R23259	Bovine parathyroid ho	8.81e-01
18	72	100.0	84	4 R23485	Porcine parathyroid h	8.81e-01
19	72	100.0	84	4 R21257	Human parathyroid hor	8.81e-01

20	72	100.0	84	4 R23424	Porcine parathyroid h	8.81e-01
21	72	100.0	84	4 R23383	Porcine parathyroid h	8.81e-01
22	72	100.0	84	5 R29568	Oxidation resistant l	8.81e-01
23	72	100.0	84	5 R29563	Oxidation resistant p	8.81e-01
24	72	100.0	84	4 R23483	Porcine parathyroid h	8.81e-01
25	72	100.0	84	25 W29420	Human parathyroid hor	8.81e-01
26	72	100.0	84	5 R29562	Oxidation resistant l	8.81e-01
27	72	100.0	84	5 R29561	Oxidation resistant p	8.81e-01
28	72	100.0	84	4 R23339	Bovine parathyroid h	8.81e-01
29	72	100.0	84	4 R23272	Bovine parathyroid ho	8.81e-01
30	72	100.0	84	4 R23301	Bovine parathyroid ho	8.81e-01
31	72	100.0	84	4 R23294	Bovine parathyroid ho	8.81e-01
32	72	100.0	84	4 R23242	Human parathyroid hor	8.81e-01
33	72	100.0	84	4 R21229	Human parathyroid hor	8.81e-01
34	72	100.0	84	4 R21181	Human parathyroid hor	8.81e-01
35	72	100.0	84	4 R23227	Human parathyroid hor	8.81e-01
36	72	100.0	84	4 R23507	Porcine parathyroid h	8.81e-01
37	72	100.0	84	4 R23264	Bovine parathyroid ho	8.81e-01
38	72	100.0	84	4 R23248	Bovine parathyroid hor	8.81e-01
39	72	100.0	84	4 R21250	Human parathyroid hor	8.81e-01
40	72	100.0	84	4 R23456	Porcine parathyroid h	8.81e-01
41	72	100.0	84	4 R23363	Bovine parathyroid ho	8.81e-01
42	72	100.0	84	4 R21180	Human parathyroid hor	8.81e-01
43	72	100.0	84	4 R23423	Porcine parathyroid h	8.81e-01
44	72	100.0	84	4 R23449	Porcine parathyroid h	8.81e-01
45	72	100.0	115	4 P40251	Protein sequence incl	8.81e-01

ALIGNMENTS

RESULT 1
 ID R58151 standard; peptide; 38 AA.
 AC R58151;
 DT 20-SEP-1994 (first entry)
 DE [Ser22]-hPTH(1-38)-OH.
 KW Human parathyroid hormone; hPTH; variant; analogue;
 KW Calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
 KW hypoparathyroidism.
 OS Synthetic.
 PN GB2269176-A.
 PD 02-FEB-1994.
 PE 12-JUL-1993; 014384.
 PR 15-JUL-1992; GB-015009.
 PR 18-DEC-1992; GB-026415.
 PR 23-DEC-1992; GB-026859.
 PR 23-DEC-1992; GB-026861.
 PR 28-JAN-1993; GB-001691.
 PR 28-JAN-1993; GB-001692.
 PR 14-APR-1993; GB-007673.
 PR 19-APR-1993; GB-008033.
 PA (SANO) SANDOZ LTD.
 PA (BAVE/) BAUER W.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F,
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H,
 PI Waelchli R, Rainer A;
 DR WPI, 94-018352/03.
 PT New active para-thyroid hormone variants - used for treating or
 preventing osteoporosis etc.
 PS Example 148; Page 40; 92pp; English.
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 SQ Sequence 38 AA;
 Query Match 100.0%; Score 72; DB 9; Length 38;
 Best Local Similarity 100.0%; Pred. No. 8.81e-01;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LQDVHNFVAL 10

RESULT 2
 ID RS8153 standard; peptide; 38 AA.
 AC RS8153;
 DT 20-SEP-1994 (first entry)
 DE [Arg26]-hPTH(1-38)-OH.
 KW Human parathyroid hormone; hPTH; variant; analogue;
 KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
 KW hypoparathyroidism.
 OS Synthetic.
 PN GB2269175-A.
 PD 02-FEB-1994.
 PF 12-JUL-1993; 014384.
 PR 15-JUL-1992; GB-015009.
 PR 18-DEC-1992; GB-026415.
 PR 23-DEC-1992; GB-026859.
 PR 23-DEC-1992; GB-026861.
 PR 28-JAN-1993; GB-001691.
 PR 14-APR-1993; GB-001692.
 PR 19-APR-1993; GB-007673.
 PA (SANO) SANDOZ LTD.
 PA (BAUER) BAUER W.
 PA (SANO) SANDOZ PATENT GMBH.
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
 PI Wepf; 94-018352/03
 PT New active para-thyroid hormone variants - used for treating or
 PS preventing osteoporosis etc.
 PS Example 150: Page 40; 92pp; English.
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 SQ Sequence 38 AA;

Query Match 100.0%; Score 72; DB 9; Length 38;
 Best Local Similarity 100.0%; Pred. No. 8.81e-01;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Caps 0;
 DB 28 lqdvhnfv al 37
 1 LQDVHNFVAL 10

Search completed: Thu Jul 30 10:50:20 1998
 Job time : 15 secs.

MUSE

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:49:12 1998; Maspar time 3.29 Seconds
111.059 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-22
Description: (1-10) from US08817547A.pep
Perfect Score: 72
Sequence: 1 LODVHNFEVAL 10

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

pl156
1:pl1 2:pl12 3:pl13 4:pl14 5:nr13d

Statistics: Mean 23.774; Variance 33.625; scale 0.707

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	72	100.0	34	5 12WE	parathyroid hormone (1.05e-03	
2	72	100.0	34	5 12WE	parathyroid hormone (1.05e-03	
3	72	100.0	34	5 12WE	parathyroid hormone (1.05e-03	
4	72	100.0	35	5 12WD	parathyroid hormone (1.05e-03	
5	72	100.0	36	5 12WB	parathyroid hormone (1.05e-03	
6	72	100.0	37	5 12WB	parathyroid hormone (1.05e-03	
7	72	100.0	37	5 12WB	parathyroid hormone (1.05e-03	
8	72	100.0	115	1 PTHU	parathyroid hormone p 1.05e-03	
9	72	100.0	115	1 PTHU	parathyroid hormone p 1.05e-03	
10	72	100.0	115	1 PTHU	parathyroid hormone p 1.05e-03	
11	72	100.0	115	1 PTHU	parathyroid hormone p 1.05e-03	
12	70	97.2	115	1 A05091	parathyroid hormone p 2.81e-03	
13	60	83.3	105	2 I51851	parathyroid hormone (3.11e-01	
14	53	73.6	34	5 12WA	parathyroid hormone (6.64e+00	
15	53	73.6	34	5 12WA	parathyroid hormone (6.64e+00	
16	53	73.6	632	2 S73824	MG242 homolog H91-ort 1.01e+01	
17	52	72.2	606	2 S13526	hydrogenase homolog, 1.35e+01	
18	51	70.8	201	2 C65188	hypothetical 22.3 kD 2.29e+01	
19	50	69.4	217	2 E70126	hypothetical protein 2.29e+01	
20	50	69.4	543	2 H40781	hypothetical 60.7K pr 2.29e+01	
21	50	69.4	543	2 S25128	61k protein - Autogra 2.29e+01	
22	50	69.4	653	2 S40449	pro-hormone converts 2.29e+01	
23	50	69.4	731	2 S28491	hypothetical protein 2.29e+01	

24	50	69.4	831	2	D36892	viPC 5'-region hypoch	2.29e+01
25 <td>49<td>68.1<td>142<td>2<td>B40535<td>clathrin-associated p<th>3.43e+01</th></td></td></td></td></td></td>	49 <td>68.1<td>142<td>2<td>B40535<td>clathrin-associated p<th>3.43e+01</th></td></td></td></td></td>	68.1 <td>142<td>2<td>B40535<td>clathrin-associated p<th>3.43e+01</th></td></td></td></td>	142 <td>2<td>B40535<td>clathrin-associated p<th>3.43e+01</th></td></td></td>	2 <td>B40535<td>clathrin-associated p<th>3.43e+01</th></td></td>	B40535 <td>clathrin-associated p<th>3.43e+01</th></td>	clathrin-associated p <th>3.43e+01</th>	3.43e+01
26 <td>49<td>68.1<td>316<td>2<td>S07569<td>protein H5 - slime mo<th>3.43e+01</th></td></td></td></td></td></td>	49 <td>68.1<td>316<td>2<td>S07569<td>protein H5 - slime mo<th>3.43e+01</th></td></td></td></td></td>	68.1 <td>316<td>2<td>S07569<td>protein H5 - slime mo<th>3.43e+01</th></td></td></td></td>	316 <td>2<td>S07569<td>protein H5 - slime mo<th>3.43e+01</th></td></td></td>	2 <td>S07569<td>protein H5 - slime mo<th>3.43e+01</th></td></td>	S07569 <td>protein H5 - slime mo<th>3.43e+01</th></td>	protein H5 - slime mo <th>3.43e+01</th>	3.43e+01
27 <td>49<td>68.1<td>455<td>2<td>A26081<td>epoxide hydrolase (EC<th>3.43e+01</th></td></td></td></td></td></td>	49 <td>68.1<td>455<td>2<td>A26081<td>epoxide hydrolase (EC<th>3.43e+01</th></td></td></td></td></td>	68.1 <td>455<td>2<td>A26081<td>epoxide hydrolase (EC<th>3.43e+01</th></td></td></td></td>	455 <td>2<td>A26081<td>epoxide hydrolase (EC<th>3.43e+01</th></td></td></td>	2 <td>A26081<td>epoxide hydrolase (EC<th>3.43e+01</th></td></td>	A26081 <td>epoxide hydrolase (EC<th>3.43e+01</th></td>	epoxide hydrolase (EC <th>3.43e+01</th>	3.43e+01
28 <td>49<td>68.1<td>1321<td>2<td>S27337<td>multidrug resistance<th>3.43e+01</th></td></td></td></td></td></td>	49 <td>68.1<td>1321<td>2<td>S27337<td>multidrug resistance<th>3.43e+01</th></td></td></td></td></td>	68.1 <td>1321<td>2<td>S27337<td>multidrug resistance<th>3.43e+01</th></td></td></td></td>	1321 <td>2<td>S27337<td>multidrug resistance<th>3.43e+01</th></td></td></td>	2 <td>S27337<td>multidrug resistance<th>3.43e+01</th></td></td>	S27337 <td>multidrug resistance<th>3.43e+01</th></td>	multidrug resistance <th>3.43e+01</th>	3.43e+01
29 <td>49<td>68.1<td>1490<td>2<td>JC5145<td>DNA (cytosine-5')-met<th>3.43e+01</th></td></td></td></td></td></td>	49 <td>68.1<td>1490<td>2<td>JC5145<td>DNA (cytosine-5')-met<th>3.43e+01</th></td></td></td></td></td>	68.1 <td>1490<td>2<td>JC5145<td>DNA (cytosine-5')-met<th>3.43e+01</th></td></td></td></td>	1490 <td>2<td>JC5145<td>DNA (cytosine-5')-met<th>3.43e+01</th></td></td></td>	2 <td>JC5145<td>DNA (cytosine-5')-met<th>3.43e+01</th></td></td>	JC5145 <td>DNA (cytosine-5')-met<th>3.43e+01</th></td>	DNA (cytosine-5')-met <th>3.43e+01</th>	3.43e+01
30 <td>49<td>68.1<td>1495<td>2<td>S22610<td>DNA (cytosine-5')-met<th>3.43e+01</th></td></td></td></td></td></td>	49 <td>68.1<td>1495<td>2<td>S22610<td>DNA (cytosine-5')-met<th>3.43e+01</th></td></td></td></td></td>	68.1 <td>1495<td>2<td>S22610<td>DNA (cytosine-5')-met<th>3.43e+01</th></td></td></td></td>	1495 <td>2<td>S22610<td>DNA (cytosine-5')-met<th>3.43e+01</th></td></td></td>	2 <td>S22610<td>DNA (cytosine-5')-met<th>3.43e+01</th></td></td>	S22610 <td>DNA (cytosine-5')-met<th>3.43e+01</th></td>	DNA (cytosine-5')-met <th>3.43e+01</th>	3.43e+01
31 <td>49<td>68.1<td>1537<td>2<td>UC4172<td>hypothetical protein<th>3.43e+01</th></td></td></td></td></td></td>	49 <td>68.1<td>1537<td>2<td>UC4172<td>hypothetical protein<th>3.43e+01</th></td></td></td></td></td>	68.1 <td>1537<td>2<td>UC4172<td>hypothetical protein<th>3.43e+01</th></td></td></td></td>	1537 <td>2<td>UC4172<td>hypothetical protein<th>3.43e+01</th></td></td></td>	2 <td>UC4172<td>hypothetical protein<th>3.43e+01</th></td></td>	UC4172 <td>hypothetical protein<th>3.43e+01</th></td>	hypothetical protein <th>3.43e+01</th>	3.43e+01
32 <td>48<td>66.7<td>145<td>5<td>S73520<td>MG41 homolog E09-ort<th>5.09e+01</th></td></td></td></td></td></td>	48 <td>66.7<td>145<td>5<td>S73520<td>MG41 homolog E09-ort<th>5.09e+01</th></td></td></td></td></td>	66.7 <td>145<td>5<td>S73520<td>MG41 homolog E09-ort<th>5.09e+01</th></td></td></td></td>	145 <td>5<td>S73520<td>MG41 homolog E09-ort<th>5.09e+01</th></td></td></td>	5 <td>S73520<td>MG41 homolog E09-ort<th>5.09e+01</th></td></td>	S73520 <td>MG41 homolog E09-ort<th>5.09e+01</th></td>	MG41 homolog E09-ort <th>5.09e+01</th>	5.09e+01
33 <td>48<td>66.7<td>145<td>5<td>1AT0<td>hypothetical protein<th>5.09e+01</th></td></td></td></td></td></td>	48 <td>66.7<td>145<td>5<td>1AT0<td>hypothetical protein<th>5.09e+01</th></td></td></td></td></td>	66.7 <td>145<td>5<td>1AT0<td>hypothetical protein<th>5.09e+01</th></td></td></td></td>	145 <td>5<td>1AT0<td>hypothetical protein<th>5.09e+01</th></td></td></td>	5 <td>1AT0<td>hypothetical protein<th>5.09e+01</th></td></td>	1AT0 <td>hypothetical protein<th>5.09e+01</th></td>	hypothetical protein <th>5.09e+01</th>	5.09e+01
34 <td>48<td>66.7<td>326<td>2<td>S76954<td>17-hedgehog 17-kDa fr<th>5.09e+01</th></td></td></td></td></td></td>	48 <td>66.7<td>326<td>2<td>S76954<td>17-hedgehog 17-kDa fr<th>5.09e+01</th></td></td></td></td></td>	66.7 <td>326<td>2<td>S76954<td>17-hedgehog 17-kDa fr<th>5.09e+01</th></td></td></td></td>	326 <td>2<td>S76954<td>17-hedgehog 17-kDa fr<th>5.09e+01</th></td></td></td>	2 <td>S76954<td>17-hedgehog 17-kDa fr<th>5.09e+01</th></td></td>	S76954 <td>17-hedgehog 17-kDa fr<th>5.09e+01</th></td>	17-hedgehog 17-kDa fr <th>5.09e+01</th>	5.09e+01
35 <td>48<td>66.7<td>328<td>2<td>A43598<td>L-lactate dehydrogena<th>5.09e+01</th></td></td></td></td></td></td>	48 <td>66.7<td>328<td>2<td>A43598<td>L-lactate dehydrogena<th>5.09e+01</th></td></td></td></td></td>	66.7 <td>328<td>2<td>A43598<td>L-lactate dehydrogena<th>5.09e+01</th></td></td></td></td>	328 <td>2<td>A43598<td>L-lactate dehydrogena<th>5.09e+01</th></td></td></td>	2 <td>A43598<td>L-lactate dehydrogena<th>5.09e+01</th></td></td>	A43598 <td>L-lactate dehydrogena<th>5.09e+01</th></td>	L-lactate dehydrogena <th>5.09e+01</th>	5.09e+01
36 <td>48<td>66.7<td>398<td>2<td>D69952<td>conserved hypothetical<th>5.09e+01</th></td></td></td></td></td></td>	48 <td>66.7<td>398<td>2<td>D69952<td>conserved hypothetical<th>5.09e+01</th></td></td></td></td></td>	66.7 <td>398<td>2<td>D69952<td>conserved hypothetical<th>5.09e+01</th></td></td></td></td>	398 <td>2<td>D69952<td>conserved hypothetical<th>5.09e+01</th></td></td></td>	2 <td>D69952<td>conserved hypothetical<th>5.09e+01</th></td></td>	D69952 <td>conserved hypothetical<th>5.09e+01</th></td>	conserved hypothetical <th>5.09e+01</th>	5.09e+01
37 <td>48<td>66.7<td>452<td>2<td>S77436<td>sigma factor s16g reg<th>5.09e+01</th></td></td></td></td></td></td>	48 <td>66.7<td>452<td>2<td>S77436<td>sigma factor s16g reg<th>5.09e+01</th></td></td></td></td></td>	66.7 <td>452<td>2<td>S77436<td>sigma factor s16g reg<th>5.09e+01</th></td></td></td></td>	452 <td>2<td>S77436<td>sigma factor s16g reg<th>5.09e+01</th></td></td></td>	2 <td>S77436<td>sigma factor s16g reg<th>5.09e+01</th></td></td>	S77436 <td>sigma factor s16g reg<th>5.09e+01</th></td>	sigma factor s16g reg <th>5.09e+01</th>	5.09e+01
38 <td>48<td>66.7<td>471<td>3<td>A43480<td>segmentation gene hed<th>5.09e+01</th></td></td></td></td></td></td>	48 <td>66.7<td>471<td>3<td>A43480<td>segmentation gene hed<th>5.09e+01</th></td></td></td></td></td>	66.7 <td>471<td>3<td>A43480<td>segmentation gene hed<th>5.09e+01</th></td></td></td></td>	471 <td>3<td>A43480<td>segmentation gene hed<th>5.09e+01</th></td></td></td>	3 <td>A43480<td>segmentation gene hed<th>5.09e+01</th></td></td>	A43480 <td>segmentation gene hed<th>5.09e+01</th></td>	segmentation gene hed <th>5.09e+01</th>	5.09e+01
39 <td>48<td>66.7<td>471<td>3<td>A46400<td>segment polarity prot<th>5.09e+01</th></td></td></td></td></td></td>	48 <td>66.7<td>471<td>3<td>A46400<td>segment polarity prot<th>5.09e+01</th></td></td></td></td></td>	66.7 <td>471<td>3<td>A46400<td>segment polarity prot<th>5.09e+01</th></td></td></td></td>	471 <td>3<td>A46400<td>segment polarity prot<th>5.09e+01</th></td></td></td>	3 <td>A46400<td>segment polarity prot<th>5.09e+01</th></td></td>	A46400 <td>segment polarity prot<th>5.09e+01</th></td>	segment polarity prot <th>5.09e+01</th>	5.09e+01
40 <td>48<td>66.7<td>653<td>2<td>S27270<td>prohormone convertase<th>5.09e+01</th></td></td></td></td></td></td>	48 <td>66.7<td>653<td>2<td>S27270<td>prohormone convertase<th>5.09e+01</th></td></td></td></td></td>	66.7 <td>653<td>2<td>S27270<td>prohormone convertase<th>5.09e+01</th></td></td></td></td>	653 <td>2<td>S27270<td>prohormone convertase<th>5.09e+01</th></td></td></td>	2 <td>S27270<td>prohormone convertase<th>5.09e+01</th></td></td>	S27270 <td>prohormone convertase<th>5.09e+01</th></td>	prohormone convertase <th>5.09e+01</th>	5.09e+01
41 <td>48<td>66.7<td>881<td>1<td>W2BE55<td>gene 55 protein - hum<th>5.09e+01</th></td></td></td></td></td></td>	48 <td>66.7<td>881<td>1<td>W2BE55<td>gene 55 protein - hum<th>5.09e+01</th></td></td></td></td></td>	66.7 <td>881<td>1<td>W2BE55<td>gene 55 protein - hum<th>5.09e+01</th></td></td></td></td>	881 <td>1<td>W2BE55<td>gene 55 protein - hum<th>5.09e+01</th></td></td></td>	1 <td>W2BE55<td>gene 55 protein - hum<th>5.09e+01</th></td></td>	W2BE55 <td>gene 55 protein - hum<th>5.09e+01</th></td>	gene 55 protein - hum <th>5.09e+01</th>	5.09e+01
42 <td>48<td>66.7<td>1318<td>1<td>H1BPD7<td>internal vitron prote<th>5.09e+01</th></td></td></td></td></td></td>	48 <td>66.7<td>1318<td>1<td>H1BPD7<td>internal vitron prote<th>5.09e+01</th></td></td></td></td></td>	66.7 <td>1318<td>1<td>H1BPD7<td>internal vitron prote<th>5.09e+01</th></td></td></td></td>	1318 <td>1<td>H1BPD7<td>internal vitron prote<th>5.09e+01</th></td></td></td>	1 <td>H1BPD7<td>internal vitron prote<th>5.09e+01</th></td></td>	H1BPD7 <td>internal vitron prote<th>5.09e+01</th></td>	internal vitron prote <th>5.09e+01</th>	5.09e+01
43 <td>48<td>66.7<td>1612<td>2<td>UC5210<td>DNA (cytosine-5')-met<th>5.09e+01</th></td></td></td></td></td></td>	48 <td>66.7<td>1612<td>2<td>UC5210<td>DNA (cytosine-5')-met<th>5.09e+01</th></td></td></td></td></td>	66.7 <td>1612<td>2<td>UC5210<td>DNA (cytosine-5')-met<th>5.09e+01</th></td></td></td></td>	1612 <td>2<td>UC5210<td>DNA (cytosine-5')-met<th>5.09e+01</th></td></td></td>	2 <td>UC5210<td>DNA (cytosine-5')-met<th>5.09e+01</th></td></td>	UC5210 <td>DNA (cytosine-5')-met<th>5.09e+01</th></td>	DNA (cytosine-5')-met <th>5.09e+01</th>	5.09e+01
44 <td>47<td>65.3<td>240<td>2<td>F4676<td>biotin synthesis prot<th>7.52e+01</th></td></td></td></td></td></td>	47 <td>65.3<td>240<td>2<td>F4676<td>biotin synthesis prot<th>7.52e+01</th></td></td></td></td></td>	65.3 <td>240<td>2<td>F4676<td>biotin synthesis prot<th>7.52e+01</th></td></td></td></td>	240 <td>2<td>F4676<td>biotin synthesis prot<th>7.52e+01</th></td></td></td>	2 <td>F4676<td>biotin synthesis prot<th>7.52e+01</th></td></td>	F4676 <td>biotin synthesis prot<th>7.52e+01</th></td>	biotin synthesis prot <th>7.52e+01</th>	7.52e+01
45 <td>47<td>65.3<td>494<td>2<td>S13101<td>cytochrome P450 c117<th>7.52e+01</th></td></td></td></td></td></td>	47 <td>65.3<td>494<td>2<td>S13101<td>cytochrome P450 c117<th>7.52e+01</th></td></td></td></td></td>	65.3 <td>494<td>2<td>S13101<td>cytochrome P450 c117<th>7.52e+01</th></td></td></td></td>	494 <td>2<td>S13101<td>cytochrome P450 c117<th>7.52e+01</th></td></td></td>	2 <td>S13101<td>cytochrome P450 c117<th>7.52e+01</th></td></td>	S13101 <td>cytochrome P450 c117<th>7.52e+01</th></td>	cytochrome P450 c117 <th>7.52e+01</th>	7.52e+01

ALIGNMENTS

RESULT	1	12WE	#type complete
ENTRY			parathyroid hormone (residues 4-37) - human
TITLE			HPTH(4-37)
ALTERNATE_NAMES			structure of human parathyroid hormone fragment 4-37, NMR 10
PDB_TITLE			Structure of human parathyroid hormone fragment 4-37, NMR 10
ORGANISM			#formal_name Homo sapiens #common_name man
REFERENCE			A67860
#authors			Roesch, P.; Marx, U.C.
#submission			submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references			PDB:12WE
REFERENCE			IN001721
#authors			Marx, U.C.
#book			In Strukturen Verschiedener Parathormonfragmente In Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996
COMMENT			Resolution: not applicable
KEYWORDS			Determination: NMR
FEATURE			hormone
SUMMARY			#region helix (right hand alpha) #length 34 #molecular-weight 4128 #checksum 5508
Query Match			100.0%; Score 72; DB 5; Length 34;
Best Local Similarity			100.0%; Pred. No. 1.05e-03;
Matches			10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	25	LODVHNFEVAL 34	
Qy	1	LODVHNFEVAL 10	
RESULT	2	12WG	#type complete
ENTRY			parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -
TITLE			synthetic
ALTERNATE_NAMES			n-succinyl-hPTH(4-37)
PDB_TITLE			succinyl human parathyroid hormone 4-37, NMR, 10 structures
ORGANISM			#formal_name synthetic
REFERENCE			A67743
#authors			Roesch, P.; Marx, U.C.
#submission			submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references			PDB:12WG
REFERENCE			TN003319
#authors			Marx, U.C.
#book			In Strukturen Verschiedener Parathormonfragmente In Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996
COMMENT			Resolution: not applicable

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COMMENT      Determination: NMR
KEYWORDS     disease mutation; hormone; signal
FEATURE      2-9      #region helix (right hand alpha)\
15-25        #region helix (right hand alpha)
SUMMARY      #length 34 #molecular-weight 4128 #checksum 5508

Query Match      100.0%; Score 72; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.05e-03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      25 LQDVHNFVAL 34
      |||||
QY      1 LQDVHNFVAL 10

Search completed: Thu Jul 30 10:49:46 1998
Job time : 34 secs.

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NWSELETH (TM)

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MPsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:47:53 1998; MasPar time 2.15 Seconds
Tabular output not generated. 116.508 Million cell updates/sec

Title: >US-08-817-547A-22
Description: (1-10) from US08817547A.pep
Perfect Score: 72
Sequence: 1 LODVHNFEVAL 10

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 24.901; Variance 27.707; scale 0.899

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Query No.	Score	Match	Length	ID	Description	Pred. No.
1	72	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	2.56e-05
2	72	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	2.56e-05
3	72	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	2.56e-05
4	72	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	2.56e-05
5	70	97.2	115	1	PTHY_RAT PARATHYROID HORMONE PR	8.57e-05
6	53	73.6	632	1	Y242_MYCPN HYPOTHETICAL PROTEIN M	1.14e+00
7	51	70.8	200	1	YIGP_ECOLI HYPOTHETICAL 22.3 KD P	3.11e+00
8	50	69.4	543	1	VP61_NPVAC 61 KD PROTEIN.	5.08e+00
9	49	68.1	142	1	EVID_SALTI VI POLYSACCHARIDE BIOS	8.24e+00
10	49	68.1	142	1	AP17_HUMAN CLATHRIN COAT ASSEMBLY	8.24e+00
11	49	68.1	142	1	AP17_RAT CLATHRIN COAT ASSEMBLY	8.24e+00
12	49	68.1	142	1	VSH5_DICDI VEGETATIVE SPECIFIC PR	8.24e+00
13	49	68.1	455	1	HYEP_RAT EPOXIDE HYDROLASE (EC	8.24e+00
14	49	68.1	1321	1	MDR1_CAHEL MULTIDRUG RESISTANCE P	8.24e+00
15	49	68.1	1495	1	MTDM_HUMAN DNA (CYTOSINE-5)-METHY	8.24e+00
16	48	66.7	136	1	V441_MYCPN HYPOTHETICAL PROTEIN M	1.32e+01
17	48	66.7	153	1	MIL1_BRARE MELANOTIN RECEPTOR TYP	1.32e+01
18	48	66.7	328	1	LDR_STRMU L-LACTATE DEHYDROGENAS	1.32e+01
19	48	66.7	398	1	YQPD_BACSU HYPOTHETICAL 45.7 KD P	1.32e+01
20	48	66.7	471	1	HH_DROME HEDGEHOG PROTEIN PRECU	1.32e+01
21	48	66.7	881	1	HELI_VZVD PROBABLE HELICASE.	1.32e+01
22	48	66.7	1318	1	VIVD_BPT7 INTERNAL VIRION PROTEI	1.32e+01
23	48	66.7	1620	1	MTDM_MOUSE DNA (CYTOSINE-5)-METHY	1.32e+01

24	47	65.3	125	1	YAMU_RHISN HYPOTHETICAL 13.3 KD P	2.11e+01
25	47	65.3	251	1	AGAI_ECOLI PUTATIVE GALACTOSAMINE	2.11e+01
26	47	65.3	274	1	CD1_STYFL T-CELL SURFACE GLYCOPR	2.11e+01
27	47	65.3	494	1	CPCN_RAT CYTOCHROME P450 IIC23	2.11e+01
28	47	65.3	589	1	KY28_MYCTU PROBABLE SERINE/THREON	2.11e+01
29	47	65.3	700	1	ADBL_YEAST PROBABLE BETA-ADAPTIN	2.11e+01
30	47	65.3	925	1	DBL_HUMAN PROTO-ONCOGENE DBL PRE	2.11e+01
31	47	65.3	1444	1	RRLP_RDV RNA-DIRECTED RNA POLYM	3.34e+01
32	46	63.9	435	1	PERC_LACLC AMINOPEPTIDASE C (EC 3	3.34e+01
33	46	63.9	469	1	NIFN_RHISN NITROGENASE IRON-MOLYB	3.34e+01
34	46	63.9	964	1	YBS9_YEAST HYPOTHETICAL 110.3 KD	3.34e+01
35	46	63.9	4344	1	DHHC_TMENT DYNENIN HEAVY CHAIN, CY	3.34e+01
36	45	62.5	104	1	YHYZ_LACHE HYPOTHETICAL 11.8 KD P	5.24e+01
37	45	62.5	120	1	YGX0_YEAST HYPOTHETICAL 14.1 KD P	5.24e+01
38	45	62.5	297	1	YMW9_YEAST OLIGOPEPTIDE TRANSPORT	5.24e+01
39	45	62.5	303	1	APPC_BACSU OLIGOPEPTIDE TRANSPORT	5.24e+01
40	45	62.5	490	1	CPGQ_MESAU CYTOCHROME P450 IIC26	5.24e+01
41	45	62.5	505	1	YXND2_CAHEL PUTATIVE SERINE CARBOX	5.24e+01
42	45	62.5	687	1	CSTA_HELPY CARBON STARVATION PROT	5.24e+01
43	45	62.5	1247	1	YMF6_CAHEL HYPOTHETICAL 139.9 KD	5.24e+01
44	45	62.5	2504	1	FAS_HUMAN FATTY ACID SYNTHASE (E	5.24e+01
45	45	62.5	2505	1	FAS_RAT FATTY ACID SYNTHASE (E	5.24e+01

ALIGNMENTS

RESULT	1	STANDARD;	PRT;	115 AA.
ID	PTHY_CANFA			
AC	P52212;			
DT	01-OCT-1996 (REL. 34, CREATED)			
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).			
GN	PTH.			
OS	CANIS FAMILIARIS (DOG).			
OC	EURAROTIA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; CARNIVORA.			
LN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PARATHYROID;			
RX	MEDLINE: 95369696.			
RA	ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,			
RA	DEWITTE J.W., CAPEN C.C.;			
RL	GENE 160:241-243(1995).			
CC	-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN			
CC	BONE AND PREVENTING THEIR RENAL EXCRETION.			
DR	EMBL: U15662; G558916; -			
DR	PROSITE: PS00335; PARATHYROID: 1.			
KW	HORMONE; SIGNAL.			
FT	SIGNAL	1	25	BY SIMILARITY.
FT	PROPEP	26	31	BY SIMILARITY.
FT	CHAIN	32	115	PARATHYROID HORMONE.
SQ	SEQUENCE	115 AA; 12957 MW; 16DEDEBC CRC32;		

Query Match 100.0%; Score 72; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.56e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	59	LODVHNFEVAL	68
Qy	1	LODVHNFEVAL	10
RESULT	2	STANDARD;	PRT; 115 AA.
ID	PTHY_BOVIN		
AC	P01268;		
DT	21-JUL-1986 (REL. 01, CREATED)		
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)		
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)		
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).		
GN	PTH.		
OS	BOS TAURUS (BOVINE).		
OC	EURAROTIA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		

Search completed: Thu Jul 30 10:47:59 1998
Job time : 6 secs.

OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 80056517.
RA KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
RL POTTS J.T. JR., RICH A.;
RN PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
RP [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 82037785.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
RP [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83105964.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL MOL. CELL. ENDOCRINOL. 28:411-424(1982).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84262483.
RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
RN GENE 28:319-329(1984).
RP [5]
RP SEQUENCE OF 26-115.
RX MEDLINE; 74142666.
RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,
RL COHN D.V.;
RN PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
RP [6]
RP SEQUENCE OF 32-115.
RX MEDLINE; 71076162.
RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,
RL AURBACH G.D., POTTS J.T. JR.;
RN HOPPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).
RP [7]
RP SEQUENCE OF 32-115.
RX MEDLINE; 71063634.
RA BREWER H.B. JR., RONAN R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE; 71091588.
RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
RL DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;
RN PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL; J00106; G85; -;
DR EMBL; J00023; G163641; -;
DR EMBL; J00024; G163643; -;
DR EMBL; J00024; E18249; ALT_SEQ.
DR EMBL; K01938; E18250; ALT_INIT.
DR EMBL; M25082; G163647; -;
DR PIR; A01534; PTBO.
DR PIR; A24949; A24949.
DR PROSITE; PS00335; PARATHYROID; 1.
KW HORMONE; SIGNAL.
FT SIGNAL 1 25
FT PROPER 26 31
FT CHAIN 32 115
FT CONFLICT 106 106
FT SEQUENCE 115 AA; 12980 MW; 673EA5F2 CRC32;
V -> G (IN REF. 4).
PARATHYROID HORMONE.
Query Match 100.0%; Score 72; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.56e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 59 LODVNFVAL 68
QY 1 LODVNFVAL 10

W O S E H
(TM)

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MSrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:48:18 1998; MasPar time 3.79 Seconds
Tabular output not generated. 111.185 Million cell updates/sec

Title: >US-08-817-547A-22
Description: (1-10) from US08817547A.pep
Perfect Score: 72
Sequence: 1 LODVHNFVAL 10

Scoring table:
PAM 150
Gap 15

Searched: 140542 seqs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptemb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 23.635; Variance 29.603; scale 0.798
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	60	83.3	105 10	063473	PARATHYROID HORMONE (F	8.41e-02
2	57	79.2	207 11	039628	ORF36L.	3.80e-01
3	54	75.0	993 3	017162	VINCULIN.	1.64e+00
4	52	72.2	345 9	P95793	STBA.	4.22e+00
5	52	72.2	606 9	046606	HYD GAMMA.	4.22e+00
6	50	69.4	653 3	016872	PREPRO-HORMONE CONVERT	1.06e+01
7	50	69.4	653 3	008845	NEUROENDOCRINE CONVERT	1.06e+01
8	50	69.4	653 3	016973	PC2.	1.06e+01
9	49	68.1	142 3	019123	SIMILARITY TO CLATHRIN	1.67e+01
10	49	68.1	207 4	029495	ARYLALKYLAMINE N-ACETY	1.67e+01
11	49	68.1	227 4	028974	CYTOSOLIC P450 2C33V3	1.67e+01
12	49	68.1	227 4	028873	CYTOSOLIC P450 2C33V2	1.67e+01
13	49	68.1	227 4	028972	CYTOSOLIC P450 2C33V1	1.67e+01
14	49	68.1	229 3	019742	SIMILAR TO SER/THR PRO	1.67e+01
15	49	68.1	455 10	P97869	MICROSOMAL EPOXIDE HYD	1.67e+01
16	49	68.1	1190 3	020187	F39B1.1 (FRAGMENT).	1.67e+01
17	49	68.1	1321 3	021349	ROB87.9.	1.67e+01
18	49	68.1	1480 12	P79822	MODIFICATION METHYLASE	1.67e+01
19	49	68.1	1537 12	P92072	MODIFICATION METHYLASE	1.67e+01
20	48	66.7	117 11	084562	GENOME, PARTIAL SEQUEN	2.61e+01

21	48	66.7	326 9	P74746	HYPOTHETICAL 36.0 KD P	2.61e+01
22	48	66.7	377 3	017273	T27A1.2 PROTEIN.	2.61e+01
23	48	66.7	440 9	055301	COTR GENE (ORF440), CO	2.61e+01
24	48	66.7	452 9	P73256	SIGNA FACTOR SIBG REGU	2.61e+01
25	48	66.7	516 3	018198	SIMILAR TO K12H4.7 AND	2.61e+01
26	48	66.7	542 11	011448	VP78.	2.61e+01
27	48	66.7	653 3	025409	STAGNALIS LPC2.	2.61e+01
28	48	66.7	708 2	092542	MYELOBLAST KIAA0253 (F	2.61e+01
29	48	66.7	787 9	032797	PYRUVATE FORMATE-LYASE	2.61e+01
30	48	66.7	787 9	032799	PYRUVATE FORMATE-LYASE	2.61e+01
31	48	66.7	1149 3	023315	ZC434.5	2.61e+01
32	48	66.7	1612 3	027746	MODIFICATION METHYLASE	2.61e+01
33	47	65.3	207 4	002785	ARYLALKYLAMINE-N-ACETY	4.04e+01
34	47	65.3	240 9	025846	BIOTIN SYNTHESIS PROTE	4.04e+01
35	47	65.3	485 1	005160	ALPHA-AGGLUTININ (AG-A	4.04e+01
36	47	65.3	494 10	064534	CYTOSOLIC P450 (EC 1.	4.04e+01
37	47	65.3	620 10	035488	VERY-LONG-CHAIN ACYL-C	4.04e+01
38	47	65.3	939 3	015799	STRAIN DD2 HEAT SHOCK	4.04e+01
39	47	65.3	939 3	015790	STRAIN 7G8 CG9 (CG9) A	4.04e+01
40	47	65.3	950 3	015788	STRAIN HB3 CG9 (CG9) A	4.04e+01
41	47	65.3	1444 11	098631	RNA-DEPENDENT RNA POLY	4.04e+01
42	46	63.9	402 12	042479	FERRICHELATASE (EC 4.9	6.22e+01
43	46	63.9	709 3	015783	HYBRID HISTIDINE KINAS	6.22e+01
44	46	63.9	1758 3	022830	SIMILAR TO HUMAN SREBP	6.22e+01
45	46	63.9	1825 10	P97394	ACTIN-CROSSLINKING PRO	6.22e+01

ALIGNMENTS

RESULT 1	PRELIMINARY; PRT; 105 AA.
ID 063473;	
AC 063473;	
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)	
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)	
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)	
DE PARATHYROID HORMONE (FRAGMENT).	
GN PTH.	
OS RATTUS NORVEGICUS (RAT).	
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
CC EUTHERIA; RODENTIA.	
RN [1]	
RP SEQUENCE FROM N.A.	
RC TISSUE-FIBROID, AND PARATHYROID;	
RA SCHMEITZER H.J., GROSS G., MAYER H.;	
RL ADV. GENE TECHNOL. 21:228-229(1984).	
DR EMBL; M54875; G601933; -	
FT NON-TER 1	
SQ SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;	

Query Match 83.3%; Score 60; DB 10; Length 105;
Best Local Similarity 80.0%; Pred. No. 8.41e-02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 49	LODVHNFVAL 58
QY 1	LODVHNFVAL 10
RESULT 2	PRELIMINARY; PRT; 207 AA.
ID 039628;	
AC 039628;	
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)	
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)	
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)	
DE ORF36L.	
OS CYDIA POMONELLA GRANDULOVIRUS.	
OC VIRUSES; DSDNA VIRUSES, NO RNA STAGE; BACULOVIRIDAE; GRANDULOVIRUS.	
RN [1]	
RP SEQUENCE FROM N.A.	
RA TEHLE J.A., VAN DER LINDEN I.F.A., VLAK J.M.;	
RL VIRUS RES. 0:0-0(1997)	
DR EMBL; AF002732; G2232189; -	
SQ SEQUENCE 207 AA; 23915 MW; D2F0E988 CRC32;	

Query Match 79.2%; Score 57; DB 11; Length 207;
 Best Local Similarity 75.0%; Pred. No. 3.80e-01;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Db 145 LOEVHDFV 152
 ||:||:
 QY 1 LODVHNFV 8

Search completed: Thu Jul 30 10:48:55 1998
 Job time : 37 secs.

WORLDWIDE
(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:52:34 1998; MasPar time 2.61 Seconds
Tabular output not generated. 52.799 Million cell updates/sec

Title: >US-08-817-547A-23
Description: (1-9) from US08817547A.pep
Perfect Score: 64
Sequence: 1 QDVHNFVAL 9

Scoring table: PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 16.221; Variance 50.458; scale 0.321
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description	Pred. No.
1	64	100.0	38	9	R58151	[Ser22]-hPTH(1-38)-OH	1.84e+00
2	64	100.0	38	9	R58142	[Asn21]-hPTH(1-38)-OH	1.84e+00
3	64	100.0	38	9	R58140	[Phe21]-hPTH(1-38)-OH	1.84e+00
4	64	100.0	38	9	R58129	[His19]-hPTH(1-38)-OH	1.84e+00
5	64	100.0	38	9	R58133	[Asp19]-hPTH(1-38)-OH	1.84e+00
6	64	100.0	44	26	P210015	Human parathyroid hor	1.84e+00
7	64	100.0	47	25	W21946	Fusion protein compri	1.84e+00
8	64	100.0	84	27	W25687	Human parathyroid hor	1.84e+00
9	64	100.0	84	4	R23237	Human parathyroid hor	1.84e+00
10	64	100.0	84	4	R21192	Human parathyroid hor	1.84e+00
11	64	100.0	84	4	R23309	Bovine parathyroid hor	1.84e+00
12	64	100.0	84	4	R21199	Human parathyroid hor	1.84e+00
13	64	100.0	84	4	R23276	Bovine parathyroid hor	1.84e+00
14	64	100.0	84	4	R21254	Human parathyroid hor	1.84e+00
15	64	100.0	84	4	R23429	Porcine parathyroid h	1.84e+00
16	64	100.0	84	4	R23259	Bovine parathyroid h	1.84e+00
17	64	100.0	84	4	R23492	Porcine parathyroid h	1.84e+00
18	64	100.0	84	4	R23493	Porcine parathyroid h	1.84e+00
19	64	100.0	84	4	R23424	Porcine parathyroid h	1.84e+00

20	64	100.0	84	4	R23383	Porcine parathyroid h	1.84e+00
21	64	100.0	84	5	R29568	Oxidation resistant p	1.84e+00
22	64	100.0	84	5	R29563	Oxidation resistant p	1.84e+00
23	64	100.0	84	4	R21240	Human parathyroid hor	1.84e+00
24	64	100.0	84	25	W29420	Human parathyroid hor	1.84e+00
25	64	100.0	84	5	R29562	Oxidation resistant p	1.84e+00
26	64	100.0	84	5	R29561	Oxidation resistant p	1.84e+00
27	64	100.0	84	4	R21250	Human parathyroid hor	1.84e+00
28	64	100.0	84	4	R21181	Human parathyroid hor	1.84e+00
29	64	100.0	84	4	R23272	Bovine parathyroid hor	1.84e+00
30	64	100.0	84	4	R23242	Human parathyroid hor	1.84e+00
31	64	100.0	84	4	R23339	Bovine parathyroid hor	1.84e+00
32	64	100.0	84	4	R23248	Human parathyroid hor	1.84e+00
33	64	100.0	84	4	R23227	Human parathyroid hor	1.84e+00
34	64	100.0	84	4	R23232	Human parathyroid hor	1.84e+00
35	64	100.0	84	4	R21217	Human parathyroid hor	1.84e+00
36	64	100.0	84	4	R23279	Bovine parathyroid hor	1.84e+00
37	64	100.0	84	4	R23278	Bovine parathyroid hor	1.84e+00
38	64	100.0	84	4	R23433	Porcine parathyroid h	1.84e+00
39	64	100.0	84	4	R23456	Porcine parathyroid h	1.84e+00
40	64	100.0	84	4	R23363	Bovine parathyroid hor	1.84e+00
41	64	100.0	84	4	R21210	Human parathyroid hor	1.84e+00
42	64	100.0	84	4	R21211	Human parathyroid hor	1.84e+00
43	64	100.0	84	4	R23449	Porcine parathyroid h	1.84e+00
44	64	100.0	115	4	P40251	Protein sequence incl	1.84e+00
45	64	100.0	229	9	R47971	Sequence of a full-le	1.84e+00

ALIGNMENTS

RESULT 1
ID R58151 standard; peptide: 38 AA.

AC R58151:
DR 20-SEP-1994 (first entry)
DE [Ser22]-hPTH(1-38)-OH.
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
PN GB269176-A.
PD 02-FEB-1994.
PE 12-JUL-1993; 014384.
PF 15-VUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (SANO) SANDOZ LTD.
PA (BAUE/) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERM GBS MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Waelchli R, Rainer A;
DR WPI, 94-018352/03.
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 148: Page 40; 92pp: English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 38 AA:

Query Match 100.0%; Score 64; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.84e+00;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 29 qdvhnfval 37

QY 1 QDVHNFVAL 9

RESULT 2
ID R58142 standard; peptide; 38 AA.
AC R58142;
DT 20-SEP-1994 (first entry)
DE [asn21]-hPTH(1-38)-OH.
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
PN GB269176-A.
PD 02-FEB-1994.
PF 12-JUL-1993; 014384.
PR 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (SANO) SANDOZ LTD.
PA (BAUER) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F,
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Waelchli R, Rainer A;
DR WPI: 94-018352/03.
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 139; Page 40; 92pp; English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 38 AA;

Query Match 100.0%; Score 64; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.84e+00;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 29 qdvhnfval 37
1 QDVHNFVAL 9

Search completed: Thu Jul 30 10:52:49 1998
Job time : 15 secs.


```

COMMENT      Determination: NMR
KEYWORDS     disease mutation; hormone; signal
FEATURE      2-9      #region helix (right hand alpha)\
               15-25   #region helix (right hand alpha)
SUMMARY      #length 34 #molecular-weight 4128 #checksum 5508

Query Match      100.0%; Score 64; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.27e-03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB      26 QDVHNFVAL 34
QY      1 QDVHNFVAL 9

Search completed: Thu Jul 30 10:52:17 1998
Job time : 26 secs.

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WATERMAN (TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:50:38 1998; MasPar time 2.13 Seconds
106.097 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-23
Description: (1-9) from US08817547A.pep
Perfect Score: 64
Sequence: 1 QDVHNFVAL 9

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 23.654; Variance 24.782; scale 0.954

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	64	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	3.54e-04
2	64	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	3.54e-04
3	64	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	3.54e-04
4	64	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	3.54e-04
5	62	96.9	115	1	PTHY_RAT PARATHYROID HORMONE PR	1.22e-03
6	49	76.6	200	1	YIGP_ECOLI HYPOTHETICAL 22.3 KD P	2.17e+00
7	48	75.0	136	1	Y441_MYCPN HYPOTHETICAL PROTEIN M	3.67e+00
8	48	75.0	153	1	ML11_BRARE MELATONIN RECEPTOR TYP	3.67e+00
9	47	73.4	274	1	CDL_SYLFL T-CELL SURFACE GLYCOPR	6.15e+00
10	47	73.4	104	1	YHV2_LACHE HYPOTHETICAL 11.8 KD P	1.68e+01
11	45	70.3	252	1	TPIS_SCHJA TRIOSEPHOSPHATE ISOMER	1.68e+01
12	45	70.3	293	1	TPIS_SCHJA TRIOSEPHOSPHATE ISOMER	1.68e+01
13	45	70.3	257	1	YMY9_YEAST HYPOTHETICAL 34.0 KD P	1.68e+01
14	45	70.3	632	1	Y242_MYCPN HYPOTHETICAL PROTEIN M	1.68e+01
15	45	70.3	687	1	CSTA_HELPY CARBON STARVATION PROT	1.68e+01
16	45	70.3	917	1	SYL_STRAU ISOLEUCYL-TRNA SYNTHET	1.68e+01
17	45	70.3	2504	1	FAS_HUMAN FATTY ACID SYNTHASE (E	1.68e+01
18	45	70.3	2505	1	FAS_RAT FATTY ACID SYNTHASE (E	1.68e+01
19	45	68.8	227	1	UBI_DROME UBIQUITIN CARBOXYL-TER	2.75e+01
20	44	68.8	505	1	Y4XG_RHISN ACETYL-COENZYME A SYNT	2.75e+01
21	44	68.8	669	1	ACSA_PENCH ACETYL-COENZYME A SYNT	2.75e+01
22	44	68.8	670	1	ACSA_EMENI ACETYL-COENZYME A SYNT	2.75e+01
23	44	68.8	670	1	ACSA_EMENI ACETYL-COENZYME A SYNT	2.75e+01

24	44	68.8	992	1	Y254_HUMAN HYPOTHETICAL PROTEIN K	2.75e+01
25	44	68.8	2133	1	FAB_FIG CONJUNCTION FACTOR VII	2.75e+01
26	43	67.2	117	1	KVSH_MOUSE IG KAPPA CHAIN PRECURS	4.43e+01
27	43	67.2	219	1	RPIA_HAIEIN RIBOSE 5-PHOSPHATE ISO	4.43e+01
28	43	67.2	264	1	YOHG_BACSU HYPOTHETICAL 30.8 KD P	4.43e+01
29	43	67.2	302	1	D3D2_HUMAN 3,2-TRANS-ENOYL-COA IS	4.43e+01
30	43	67.2	309	1	VPE2_MRDV PROBABLE NONSTRUCTURAL	4.43e+01
31	43	67.2	411	1	Y1BB_ECOLI HYPOTHETICAL 45.7 KD P	4.43e+01
32	43	67.2	444	1	CADB_ECOLI PROBABLE CADDAVERINE/LY	4.43e+01
33	43	67.2	447	1	CLUS_RAT CLUSTERIN PRECURSOR (S	4.43e+01
34	43	67.2	449	1	CEP1_MACFA SERINE HYDROXYMETHYLTR	4.43e+01
35	43	67.2	483	1	CEP1_MACFA SERINE HYDROXYMETHYLTR	4.43e+01
36	43	67.2	483	1	CRCO_MESAU CYTOCHROME P450 IIC26	4.43e+01
37	43	67.2	490	1	CRCO_MESAU CYTOCHROME P450 IIC25	4.43e+01
38	43	67.2	490	1	CPG6_RAT CYTOCHROME P450 IIC6 (4.43e+01
39	43	67.2	493	1	CEP1_HUMAN CYTOCHROME P450 IIE1 (4.43e+01
40	43	67.2	493	1	CEP1_MESAU CYTOCHROME P450 IIE1 (4.43e+01
41	43	67.2	741	1	CH12_YEAST CULLIN HOMOLOG 1 (CUL-	4.43e+01
42	43	67.2	752	1	CUL1_HUMAN HYPOTHETICAL 112.7 KD	4.43e+01
43	43	67.2	962	1	YAXA_SCHPO FERREDOXIN-DEPENDENT G	4.43e+01
44	43	67.2	1550	1	GLTB_SYNY3 FATTY ACID SYNTHASE (E	4.43e+01
45	43	67.2	2511	1	FAS_CHICK FATTY ACID SYNTHASE (E	4.43e+01

ALIGNMENTS

RESULT	ID	PTHY_CANFA	STANDARD	PRT	115 AA.
AC	P52212				
DT	01-OCT-1996	(REL. 34, CREATED)			
DT	01-OCT-1996	(REL. 34, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996	(REL. 34, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).				
GN	PTH.				
OS	CANIS FAMILIARIS (DOG).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
CC	EUPHERIA; CARNIVORA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-PARATHYROID.				
RX	MEDLINE: 95369696.				
RA	ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,				
RA	DEWITTE J.W., CAPEN C.C.,				
RL	GENE 160:241-243(1995).				
CC	-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN				
CC	BONE AND PREVENTING THEIR RENAL EXCRETION.				
DR	EMBL: U15662; G558916; -				
DR	PROSITE: PS00335; PARATHYROID: 1.				
KW	HORMONE; SIGNAL.				
FT	SIGNAL	1	25	BY SIMILARITY.	
FT	PROPEP	26	31	BY SIMILARITY.	
FT	CHAIN	32	115	PARATHYROID HORMONE.	
SO	SEQUENCE	115 AA;	12957 MW;	16ED0BC CRC32;	
Query Match					
Best Local Similarity 100.0%; Score 64; DB 1; Length 115;					
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
DB	60 QDVHNFVAL	68			
QY	1 QDVHNFVAL	9			
RESULT 2					
AC	PTHY_BOVIN	STANDARD;	PRT;	115 AA.	
DT	21-JUL-1986	(REL. 01, CREATED)			
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).				
GN	PTH.				
OS	BOS TAURUS (BOVINE).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				

Search completed: Thu Jul 30 10:50:45 1998
Job time : 7 secs.

```

OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 80056617.
RA KRONENBERG H.M., MCDEVITT B.E., MAJCOUB J.A., NATHANS J., SHARP P.A.,
RL POTTS J.T., JR., RICH A.;
RN PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 82037785.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83105964.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL MOL. CELL. ENDOCRINOL. 28:411-424(1982).
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84262483.
RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
RL GENE 28:319-329(1984).
[5]
RP SEQUENCE OF 26-115.
RX MEDLINE; 74142666.
RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T., JR.,
RL COHN D.V.;
RN PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
[6]
RP SEQUENCE OF 32-115.
RX MEDLINE; 71076162.
RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,
RL AURBACH G.D., POTTS J.T., JR.;
RN HOPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).
[7]
RP SEQUENCE OF 32-115.
RX MEDLINE; 71063634.
RA BREWER H.B., JR., ROMAN R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
[8]
RP SYNTHESIS OF 32-65.
RX MEDLINE; 71091588.
RA POTTS J.T., JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
RL DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;
RN PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
[9]
RP FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL; J00106; G85; -;
DR EMBL; J00023; G163641; -;
DR EMBL; J00024; G163643; -;
DR EMBL; J00024; E18249; ALT_SEQ.
DR EMBL; J00024; E18250; ALT_INIT.
DR EMBL; K01938; G163647; -;
DR EMBL; M25082; G163645; -;
DR PIR; A01534; PTBO.
DR PIR; A24949; A24949.
DR PROSITE; PS00335; PARATHYROID; 1.
KW HORMONE; SIGNAL.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 PARATHYROID HORMONE.
FT CONFLICT 106 106 V -> G (IN REF. 4).
SQ SEQUENCE 115 AA; 12980 MW; 673EA5F2 CRC32;

Query Match 100.0%; Score 64; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 3,54e-04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 60 QDVHNFVAL 68
QY 1 QDVHNFVAL 9

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MUSEUM
(TM)

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Muscle_p protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:51:03 1998; MasPar time 3.73 Seconds
101.507 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-23
Description: (1-9) from US08817547A.pep
Perfect Score: 64
Sequence: 1 QDVHNFVAL 9

Scoring table: PAM 150
Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: spiremb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_ricent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 22.521; Variance 26.779; scale 0.841

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	52	81.3	105 10	063473	PARATHYROID HORMONE (F	1.20e+00
2	52	81.3	345 9	P95793	STBA.	1.20e+00
3	49	76.6	207 11	039638	ORE36L.	5.36e+00
4	49	76.6	455 10	P97869	MICROSOMAL EPOXIDE HYD	5.36e+00
5	48	75.0	117 11	084562	GENOME, PARTIAL, SEQUEN	8.71e+00
6	48	75.0	377 3	017273	T27A1.2 PROTEIN.	8.71e+00
7	46	71.9	535 8	P93479	BERBERINE BRIDGE ENZYM	2.25e+01
8	46	71.9	620 3	001909	SIMILARITY TO MULTIPLE	2.25e+01
9	46	71.9	993 3	017162	VINCULIN.	2.25e+01
10	45	70.3	163 9	035962	PEPTIDYL-PROLYL CIS-TR	3.58e+01
11	45	70.3	552 9	006642	POTASSIUM FLAVIN-ADENIN	3.58e+01
12	45	70.3	2505 10	063577	FATTY ACID SYNTHASE. (E	3.58e+01
13	45	70.3	2509 2	016702	FATTY ACID SYNTHASE. (E	3.58e+01
14	44	68.8	140 9	028710	HYPOTHETICAL. 15.7 KD P	5.64e+01
15	44	68.8	155 12	090432	OLFACTORY RECEPTOR (FR	5.64e+01
16	44	68.8	211 9	P76343	FROM BASES 2030342 TO	5.64e+01
17	44	68.8	255 9	060031	TRIOSEPHOSPHATE ISOMER	5.64e+01
18	44	68.8	263 3	020557	COSMID F48B9.	5.64e+01
19	44	68.8	315 10	006832	VBEFA2 PROTEIN.	5.64e+01
20	44	68.8	315 11	083411	RETROVIRIDAE PROTEIN.	5.64e+01

RESULT	ID	Query Match	Score	DB ID	Description	Pred. No.
1	063473	50 QDVHNFVAL 9	81.38	105 AA	PARATHYROID HORMONE (F	1.20e+00
2	P95793	1 QDVHNFVAL 9	77.88	105 AA	STBA.	1.20e+00
3	039638	1 QDVHNFVAL 9	76.6	105 AA	ORE36L.	5.36e+00
4	P97869	1 QDVHNFVAL 9	76.6	105 AA	MICROSOMAL EPOXIDE HYD	5.36e+00
5	084562	1 QDVHNFVAL 9	75.0	105 AA	GENOME, PARTIAL, SEQUEN	8.71e+00
6	017273	1 QDVHNFVAL 9	75.0	105 AA	T27A1.2 PROTEIN.	8.71e+00
7	P93479	1 QDVHNFVAL 9	71.9	105 AA	BERBERINE BRIDGE ENZYM	2.25e+01
8	001909	1 QDVHNFVAL 9	71.9	105 AA	SIMILARITY TO MULTIPLE	2.25e+01
9	017162	1 QDVHNFVAL 9	71.9	105 AA	VINCULIN.	2.25e+01
10	035962	1 QDVHNFVAL 9	70.3	105 AA	PEPTIDYL-PROLYL CIS-TR	3.58e+01
11	006642	1 QDVHNFVAL 9	70.3	105 AA	POTASSIUM FLAVIN-ADENIN	3.58e+01
12	063577	1 QDVHNFVAL 9	70.3	105 AA	FATTY ACID SYNTHASE. (E	3.58e+01
13	016702	1 QDVHNFVAL 9	70.3	105 AA	FATTY ACID SYNTHASE. (E	3.58e+01
14	028710	1 QDVHNFVAL 9	68.8	105 AA	HYPOTHETICAL. 15.7 KD P	5.64e+01
15	090432	1 QDVHNFVAL 9	68.8	105 AA	OLFACTORY RECEPTOR (FR	5.64e+01
16	P76343	1 QDVHNFVAL 9	68.8	105 AA	FROM BASES 2030342 TO	5.64e+01
17	060031	1 QDVHNFVAL 9	68.8	105 AA	TRIOSEPHOSPHATE ISOMER	5.64e+01
18	020557	1 QDVHNFVAL 9	68.8	105 AA	COSMID F48B9.	5.64e+01
19	006832	1 QDVHNFVAL 9	68.8	105 AA	VBEFA2 PROTEIN.	5.64e+01
20	083411	1 QDVHNFVAL 9	68.8	105 AA	RETROVIRIDAE PROTEIN.	5.64e+01

ALIGNMENTS

RESULT	ID	Query Match	Score	DB ID	Description	Pred. No.
1	063473	50 QDVHNFVAL 9	81.38	105 AA	PARATHYROID HORMONE (F	1.20e+00
2	P95793	1 QDVHNFVAL 9	77.88	105 AA	STBA.	1.20e+00
3	039638	1 QDVHNFVAL 9	76.6	105 AA	ORE36L.	5.36e+00
4	P97869	1 QDVHNFVAL 9	76.6	105 AA	MICROSOMAL EPOXIDE HYD	5.36e+00
5	084562	1 QDVHNFVAL 9	75.0	105 AA	GENOME, PARTIAL, SEQUEN	8.71e+00
6	017273	1 QDVHNFVAL 9	75.0	105 AA	T27A1.2 PROTEIN.	8.71e+00
7	P93479	1 QDVHNFVAL 9	71.9	105 AA	BERBERINE BRIDGE ENZYM	2.25e+01
8	001909	1 QDVHNFVAL 9	71.9	105 AA	SIMILARITY TO MULTIPLE	2.25e+01
9	017162	1 QDVHNFVAL 9	71.9	105 AA	VINCULIN.	2.25e+01
10	035962	1 QDVHNFVAL 9	70.3	105 AA	PEPTIDYL-PROLYL CIS-TR	3.58e+01
11	006642	1 QDVHNFVAL 9	70.3	105 AA	POTASSIUM FLAVIN-ADENIN	3.58e+01
12	063577	1 QDVHNFVAL 9	70.3	105 AA	FATTY ACID SYNTHASE. (E	3.58e+01
13	016702	1 QDVHNFVAL 9	70.3	105 AA	FATTY ACID SYNTHASE. (E	3.58e+01
14	028710	1 QDVHNFVAL 9	68.8	105 AA	HYPOTHETICAL. 15.7 KD P	5.64e+01
15	090432	1 QDVHNFVAL 9	68.8	105 AA	OLFACTORY RECEPTOR (FR	5.64e+01
16	P76343	1 QDVHNFVAL 9	68.8	105 AA	FROM BASES 2030342 TO	5.64e+01
17	060031	1 QDVHNFVAL 9	68.8	105 AA	TRIOSEPHOSPHATE ISOMER	5.64e+01
18	020557	1 QDVHNFVAL 9	68.8	105 AA	COSMID F48B9.	5.64e+01
19	006832	1 QDVHNFVAL 9	68.8	105 AA	VBEFA2 PROTEIN.	5.64e+01
20	083411	1 QDVHNFVAL 9	68.8	105 AA	RETROVIRIDAE PROTEIN.	5.64e+01

Thu Jul 30 13:38:06 1998

US-08-817-547A-23.ispt

Page 2

RL SUBMITTED (DEC-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U59131; G1695865; -
KM PLASMID.
SQ SEQUENCE 345 AA; 38433 MW; E194251E CRC32;

Query Match 81.3%; Score 52; DB 9; Length 345;
Best Local Similarity 77.8%; Pred. No. 1.20e+00;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 116 QDVHLEFVL 124
||| |||
QY 1 QDVHNEFVAL 9

Search completed: Thu Jul 30 10:51:32 1998
Job time : 29 secs.

WIRE (TW)

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Masrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:55:02 1998; MasPar time 2.60 Seconds
Tabular output not generated. 47.193 Million cell updates/sec

Title: >US-08-817-547A-24
Description: (1-8) from US08817547A.pep
Perfect Score: 57
Sequence: 1 DVHNFVAL 8

Scoring table: PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseg31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 15.692; Variance 45.953; scale 0.341

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	57	100.0	38	9	R58151 [Ser22]-hPTH(1-38)-OH	5.52e+00
2	57	100.0	38	9	R58142 [Asn21]-hPTH(1-38)-OH	5.52e+00
3	57	100.0	38	9	R58140 [Phe21]-hPTH(1-38)-OH	5.52e+00
4	57	100.0	38	9	R58129 [His19]-hPTH(1-38)-OH	5.52e+00
5	57	100.0	38	9	R58133 [Asp19]-hPTH(1-38)-OH	5.52e+00
6	57	100.0	44	26	P30015 Human parathyroid hor	5.52e+00
7	57	100.0	47	25	W21946 Fusion protein compri	5.52e+00
8	57	100.0	84	27	W25687 Human parathyroid hor	5.52e+00
9	57	100.0	84	4	R23227 Human parathyroid hor	5.52e+00
10	57	100.0	84	4	R2181 Human parathyroid hor	5.52e+00
11	57	100.0	84	4	R23276 Human parathyroid hor	5.52e+00
12	57	100.0	84	4	R21254 Human parathyroid hor	5.52e+00
13	57	100.0	84	4	R23429 Porcine parathyroid h	5.52e+00
14	57	100.0	84	4	R23259 Bovine parathyroid h	5.52e+00
15	57	100.0	84	4	R23444 Porcine parathyroid h	5.52e+00
16	57	100.0	84	4	R23281 Bovine parathyroid ho	5.52e+00
17	57	100.0	84	4	R23424 Porcine parathyroid h	5.52e+00
18	57	100.0	84	4	R23383 Porcine parathyroid h	5.52e+00
19	57	100.0	84	4	R21161 Human parathyroid hor	5.52e+00

20	57	100.0	84	5	R29563 Oxidation resistant P	5.52e+00
21	57	100.0	84	4	R21241 Human parathyroid hor	5.52e+00
22	57	100.0	84	4	R21240 Human parathyroid hor	5.52e+00
23	57	100.0	84	25	W29420 Human parathyroid hor	5.52e+00
24	57	100.0	84	5	R29562 Oxidation resistant I	5.52e+00
25	57	100.0	84	5	R29561 Oxidation resistant P	5.52e+00
26	57	100.0	84	4	R23493 Porcine parathyroid h	5.52e+00
27	57	100.0	84	4	R23492 Porcine parathyroid h	5.52e+00
28	57	100.0	84	4	R23309 Bovine parathyroid ho	5.52e+00
29	57	100.0	84	4	R21199 Human parathyroid hor	5.52e+00
30	57	100.0	84	4	R21187 Human parathyroid hor	5.52e+00
31	57	100.0	84	4	R21219 Human parathyroid hor	5.52e+00
32	57	100.0	84	4	R21250 Human parathyroid hor	5.52e+00
33	57	100.0	84	4	R23248 Human parathyroid hor	5.52e+00
34	57	100.0	84	4	R23433 Porcine parathyroid h	5.52e+00
35	57	100.0	84	4	R23392 Porcine parathyroid h	5.52e+00
36	57	100.0	84	4	R23279 Bovine parathyroid ho	5.52e+00
37	57	100.0	84	4	R23278 Bovine parathyroid ho	5.52e+00
38	57	100.0	84	4	R23374 Bovine parathyroid ho	5.52e+00
39	57	100.0	84	4	R23240 Human parathyroid hor	5.52e+00
40	57	100.0	84	4	R23456 Porcine parathyroid h	5.52e+00
41	57	100.0	84	4	R23363 Bovine parathyroid ho	5.52e+00
42	57	100.0	84	4	R21210 Human parathyroid hor	5.52e+00
43	57	100.0	84	4	R21211 Human parathyroid hor	5.52e+00
44	57	100.0	84	4	R23449 Porcine parathyroid h	5.52e+00
45	57	100.0	229	9	R47971 Sequence of a full-le	5.52e+00

ALIGNMENTS

RESULT 1
ID R58151 standard; peptide; 38 AA.
AC R58151;
DT 20-SEP-1994 (first entry)
DE [Ser22]-hPTH(1-38)-OH.
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
PN GB2269176-A.
PD 02-FEB-1994.
PF 12-JUL-1993; 014384.
PI 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (SANO) SANDOZ LTD.
PA (BAUE/) BAUER W.
PA (SANO) SANDOZ-PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNG VERW GES MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F,
PI Gombert F, Gram H, Lewis I, Ramage F, Schneider H;
PI Waelchli R, Rainer A;
DR WPI: 94-018352/03.
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 146, page 40; 92pp; English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 38 AA:

Query Match 100.0%; Score 57; DB 9; Length 38;
Best local Similarity 100.0%; Pred. No. 5.52e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 30 dvhnfval 37

QY 1 DVHNFVAL 8

RESULT 2
ID R58142 standard; peptide; 38 AA.

AC R58142;
DT 20-SEP-1994 (first entry)
DE [Asn21]-hPTH(1-38)-OH
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
PN GB269176-A.

PD 02-FEB-1994.
PE 12-JUL-1993; 014384.
PR 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-001691.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.

PA (SANO) SANDOZ LTD.
PA (BAUE/) BAUER W.
PA (SANO) SANDOZ-PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Waelchli R, Rainer A;
DR WPI: 94-018352/03.
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 139, Page 40: 92pp: English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 38 AA;

Query Match 100.0%; Score 57; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 5.52e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 30 dvhmfval 37
1 DVHNFVAL 8

Search completed: Thu Jul 30 10:55:16 1998
Job time : 14 secs.

MUSEUM
(TM)

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MPsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:54:14 1998; MasPar time 3.34 Seconds
Tabular output not generated. 87.598 Million cell updates/sec

Title: >US-08-817-547A-24
Description: (1-8) from US08817547A.pep
Perfect Score: 57
Sequence: 1 DVHNFVAL 8

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr56
1:plr1 2:plr2 3:plr3 4:plr4 5:nrl3d

Statistics: Mean 21.941; Variance 28.147; scale 0.780

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	57	100.0	34	5 12WE	parathyroid hormone (1.14e-01	
2	57	100.0	34	5 12WE	parathyroid hormone (1.14e-01	
3	57	100.0	34	5 12WE	parathyroid hormone (1.14e-01	
4	57	100.0	34	5 12WE	parathyroid hormone (1.14e-01	
5	57	100.0	36	5 12WB	parathyroid hormone (1.14e-01	
6	57	100.0	37	5 12WB	parathyroid hormone (1.14e-01	
7	57	100.0	37	5 12WB	parathyroid hormone (1.14e-01	
8	57	100.0	37	5 12WB	parathyroid hormone (1.14e-01	
9	57	100.0	115	1 PTRU	parathyroid hormone (1.14e-01	
10	57	100.0	115	1 PTRU	parathyroid hormone (1.14e-01	
11	57	100.0	115	1 PTRU	parathyroid hormone (1.14e-01	
12	55	96.5	115	1 PTRU	parathyroid hormone (1.14e-01	
13	47	82.5	136	2 S73520	parathyroid hormone (1.14e-01	
14	46	80.7	201	2 C65188	MG441 homolog E09-ort	
15	46	80.7	274	2 B45887	hypothetical 22.3 kd	
16	46	80.7	1520	2 G69634	leukocyte differential	
17	45	78.9	104	2 B37145	glutamate synthase (1	
18	45	78.9	105	2 B37145	hypothetical 12k hlv	
19	45	78.9	297	2 S55085	parathyroid hormone -	
20	45	78.9	687	2 H64665	hypothetical protein	
21	45	78.9	2504	2 B57788	carbon starvation pro	
22	45	78.9	2504	2 A57788	fatty-acid synthase (
23	45	78.9	2505	1 XYRTFA	fatty-acid synthase (

24	45	78.9	2509	2 G01880	fatty-acid synthase (3.39e-01
25	44	77.2	140	2 A69445	hypothetical protein	5.24e-01
26	44	77.2	227	2 S33956	ubiquitin thiolester	5.24e-01
27	44	77.2	632	2 S73824	MG242 homolog H91.orf	1.22e+02
28	43	75.4	219	2 B64153	ribose-5-phosphate is	8.03e+01
29	43	75.4	302	2 A55722	dodecenoyl-CoA Delta-	8.03e+01
30	43	75.4	309	2 B35545	hypothetical protein	8.03e+01
31	42	75.4	444	2 A41842	lysine/cadaverine ant	8.03e+01
32	43	75.4	760	2 I51720	probable DNA helicase	8.03e+01
33	43	75.4	962	2 S67385	hypothetical protein	8.03e+01
34	43	75.4	2512	1 XYCHFA	fatty-acid synthase (8.03e+01
35	42	73.7	178	5 ICTNA	cyclophilin b, chain	1.22e+02
36	42	73.7	182	5 2RMCE	cyclophilin c complex	1.22e+02
37	42	73.7	182	5 2RMCC	cyclophilin c complex	1.22e+02
38	42	73.7	182	5 2RMCG	cyclophilin c complex	1.22e+02
39	42	73.7	182	5 2RMCA	cyclophilin c complex	1.22e+02
40	42	73.7	207	2 A40516	peptidylprolyl isomer	1.22e+02
41	42	73.7	208	1 C58UB	peptidylprolyl isomer	1.22e+02
42	42	73.7	212	1 A40047	peptidylprolyl isomer	1.22e+02
43	42	73.7	212	2 A54204	peptidylprolyl isomer	1.22e+02
44	42	73.7	316	2 S07569	protein H5 - slime mo	1.22e+02
45	42	73.7	1321	2 S27337	multidrug resistance	1.22e+02

ALIGNMENTS

RESULT	1	12WE	#type complete
ENTRY		parathyroid hormone (residues 4-37) - human	
TITLE		HPH(4-37)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 4-37, NMR 10	
PDB-TITLE		structures	
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67860	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WE	
REFERENCE		TN001721	
#authors		Marx, U.C.	
#book		In Strukturen Verschiedener Parathormonfragmente In Loesung,	
COMMENT		pp.0, Bayreuth : University of Bayreuth (thesis), 1996	
COMMENT		Resolution: not applicable	
KEYWORDS		hormone	
FEATURE			
15-25			
SUMMARY		#region helix (right hand alpha)	
		#length 34 #molecular-weight 4128 #checksum 5508	
Query Match		100.0%; Score 57; DB 5; Length 34;	
Best Local Similarity		100.0%; Pred. No. 1.14e-01;	
Matches		8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
DB	27	DVHNFVAL 34	
QY	1	DVHNFVAL 8	
RESULT	2	12WG	#type complete
ENTRY		parathyroid hormone 4-37 mutant N-TERMINAL SUCCINYLATED -	
TITLE		synthetic	
ALTERNATE_NAMES		n-succinyl-1-hph(4-37)	
PDB-TITLE		succinyl human parathyroid hormone 4-37, NMR, 10 structures	
ORGANISM		#formal_name synthetic	
REFERENCE		A67743	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WG	
REFERENCE		TN003319	
#authors		Marx, U.C.	
#book		In Strukturen Verschiedener Parathormonfragmente In Loesung,	
COMMENT		pp.0, Bayreuth : University of Bayreuth (thesis), 1996	
COMMENT		Resolution: not applicable	

COMMENT Determination: NMR
KEYWORDS disease mutation; hormone; signal
FEATURE

2-9 #region helix (right hand alpha) \
15-25 #region helix (right hand alpha) \
SUMMARY #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 57; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1,14e-01;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 DVHNEVAL 34
QY 1 DVHNEVAL 8

Search completed: Thu Jul 30 10:54:45 1998
Job time : 31 secs.

Search completed: Thu Jul 30 10:53:13 1998
Job time : 6 secs.

```
OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 80056617.
RA KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
RL POTTS J.T., JR., RICH A.;
RN PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 82037785.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 83105964.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL MOL. CELL. ENDOCRINOL. 28:411-424(1982).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE: 84262483.
RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
RL GENE 28:319-329(1984).
RN [5]
RP SEQUENCE OF 26-115.
RX MEDLINE: 74142666.
RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T., JR.,
RL COHN D.V.;
RN PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
RN [6]
RP SEQUENCE OF 32-115.
RX MEDLINE: 71076162.
RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,
RL AUBACH G.D., POTTS J.T., JR.;
RN HOPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).
RN [7]
RP SEQUENCE OF 32-115.
RX MEDLINE: 71063634.
RA BREMER H.B., JR., ROMAN R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE: 71091588.
RA POTTS J.T., JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
RL DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURECH G.D.;
RN PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
    BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL: V00106; G85; -.
DR EMBL: J00023; G163641; -.
DR EMBL: J00024; G163643; -.
DR EMBL: J00024; E18249; ALT_SEQ.
DR EMBL: J00024; E18250; ALT_INIT.
DR EMBL: K01938; G163647; -.
DR EMBL: M25082; G163645; -.
DR PIR: A01534; PTBO.
DR PIR: A24949; A24949.
DR PROSITE: PS00335; PARATHYROID: 1.
KW HORMONE; SIGNAL.
FT SIGNAL. 1 25
FT PROPEP 26 31 PARATHYROID HORMONE.
FT CHAIN 32 115 V -> G (IN REF. 4).
FT CONFLICT 106 106
SQ SEQUENCE 115 AA; 12980 MW; 673EA5F2 CRC32;

Query Match 100.0%; Score 57; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 8.14e-03;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

M O S E R
(TW)

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MPSrch_DP protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:53:31 1998; MasPar time 3.69 Seconds
Tabular output not generated. 91.336 Million cell updates/sec

Title: >US-08-817-547A-24
Description: (1-6) from US08817547A.pep
Perfect Score: 57
Sequence: 1 DVHNFVAL 8

Scoring table: PAM 150
Gap 15

Searched: 140542 seqs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: spiremb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 21.944; Variance 25.449; scale 0.862

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	46	80.7	620	3	001909	SIMILARITY TO MULTIPLE PARATHYROID HORMONE (F	1.28e+01
2	45	78.9	105	10	063473	STBA.	2.08e+01
3	45	78.9	345	9	P95793	PUTATIVE FLAVELLA-RELA	2.08e+01
4	45	78.9	552	9	006642	FATTY ACID SYNTHASE	2.08e+01
5	45	78.9	2505	10	063577	FATTY ACID SYNTHASE (E	2.08e+01
6	45	78.9	2509	2	016702	GENOME, PARTIAL SEQU	3.35e+01
7	44	77.2	117	11	084562	HYPOTHETICAL 15.7 KD P	3.35e+01
8	44	77.2	140	9	028710	SIMILAR TO S. CERVISI	3.35e+01
9	44	77.2	368	9	021158	HYPOTHETICAL 49.1 KD P	3.35e+01
10	44	77.2	473	9	024723	DELTA3, DELTA2-ENOYL-C	3.35e+01
11	43	75.4	266	2	013290	ERCC2/XPD.	5.35e+01
12	43	75.4	760	12	091941	ERCC2/XPD.	5.35e+01
13	43	75.4	932	3	017301	ERCC2/XPD.	5.35e+01
14	43	75.4	1221	3	021344	K08E7.5	5.35e+01
15	43	75.4	1283	3	018824	SIMILAR TO MUTFLRUC-R	5.35e+01
16	43	75.4	2408	2	092566	MYELOBLAST KIA0279 (F	5.35e+01
17	42	73.7	62	9	P76618	FROM BASES 27575730 TO	8.47e+01
18	42	73.7	195	9	049043	ABC TRANSPORTER (OLIGO	8.47e+01
19	42	73.7	196	3	094770	CYCLOPHILIN HOMOLOG TA	8.47e+01
20	42	73.7	207	11	039628	ORF36L.	8.47e+01

RESULT	ID	PRELIMINARY	PRT	620 AA.	ALIGNMENTS
AC	001909	001909			
DT	01-JUL-1997	(TREMBLEREL. 04, CREATED)			
DT	01-JUL-1997	(TREMBLEREL. 04, LAST SEQUENCE UPDATE)			
DT	01-JUL-1997	(TREMBLEREL. 04, LAST ANNOTATION UPDATE)			
DE	SIMILARITY TO MULTIPLE CADHERIN-TYPE REPEATS.				
GN	R10F2.2.				
OS	CANONHABDITIS ELEGANS.				
OC	EDUAROTA; METAFOA; ACCELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	SPRAIN-BRISTOL N2;				
RX	MEDLINE; 94150718.				
RA	WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,				
RA	BOFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,				
RA	CRASTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,				
RA	GARDNER A., GREEN P., HAWKINS T., HILLER L., JIRI M., JOHNSTON L.,				
RA	JONES M., KERSHAW J., KIRSTEN J., LAISNER J., LATREILLE P.,				
RA	LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,				
RA	PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SANDERS D., SHOWNKEEN R.,				
RA	SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,				
RA	THERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,				
RA	WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOLDMAN P.,				
RL	NATURE 368:32-38(1994).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	SPRAIN-BRISTOL N2;				
RA	DU Z., GATTUNG S.;				
RL	SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	SPRAIN-BRISTOL N2;				
RA	WATERSTON R.;				
RL	SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.				
DR	EMBL; AF003388; G2088851.				
SO	SEQUENCE 620 AA; 67475 MW; 17C581A5 CRC32;				

Query Match: 80.7%; Score 46; DB 3; Length 620;
Best Local Similarity 75.0%; Pred. No. 1.28e+01;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 134 DVHNFVAL 141
||| |||







QY 1 DVHNFVAL 8

```
RESULT 2
ID 063473 PRELIMINARY; PRT; 105 AA.
AC 063473;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE (FRAGMENT).
GN PTH.
OS RATIUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-THYROID, AND PARATHYROID;
RA SCHMELZER H.J., GROSS G., MAYER H.;
RL ADV. GENE TECHNOL. 21:228-229(1984).
EMB1: M54875; G601933; -.
NON_TER 1
SEQUENCE 105 AA; 11746 MM; 6AC3163E CRC32;

Query Match 78.9%; Score 45; DB 10; Length 105;
Best Local Similarity 75.0%; Pred. No. 2.08e+01;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 51 DGHNFVSL 58
QY 1 DVHNFVAL 8
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Search completed: Thu Jul 30 10:53:58 1998
Job time : 27 secs.

Thu Jul 30 13:38:07 1998

US-08-817-547A-25.rag

OY 1 VHNFEVAL 7

RESULT 2
 ID R58128 standard; peptide; 38 AA.
 AC R58128;
 DT 20-SEP-1994 (first entry)
 DE [His19]-hPTH(1-38)-OH.
 KW Human parathyroid hormone; hPTH; variant; analogue;
 KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
 KW hypoparathyroidism.
 OS Synthetic.
 PN GB2269176-A.
 PD 02-FEB-1994.
 PF 12-JUL-1993; 014384
 PR 15-JUL-1992; GB-015009.
 PR 18-DEC-1992; GB-026415.
 PR 23-DEC-1992; GB-026859.
 PR 23-DEC-1992; GB-026861.
 PR 28-JAN-1993; GB-001691.
 PR 28-JAN-1993; GB-001692.
 PR 14-APR-1993; GB-007673.
 PR 19-APR-1993; GB-008033.
 PA (SANO) SANDOZ LTD.
 PA (BAUE/) BAUER W.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F,
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H,
 PI Waelchli R, Rainer A;
 PI WPI; 94-018352/03.
 DR New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc. English.
 PS Example 126; Page 39; 92pp; English.
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 CC Sequence 38 AA;
 SQ

Query Match 100.0%; Score 51; DB 9; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.64e+01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 31 vhnfeval 37
 1 VHNFEVAL 7

Search completed: Thu Jul 30 10:57:31 1998
 Job time : 14 secs.

 Nucleotide sequence (TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
 on: Thu Jul 30 10:56:41 1998; MasPar time 3.23 Seconds
 Tabular output not generated. 79.088 Million cell updates/sec

Title: >US-08-817-547A-25
 Description: (1-7) from US08817547A.pep
 Perfect Score: 51
 Sequence: 1 VHNFEVAL 7

Scoring table: PAM 150
 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: p1r56
 1:p1r1 2:p1r2 3:p1r3 4:p1r4 5:nr13d

Statistics: Mean 21.152; Variance 25.908; scale 0.816

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	51	100.0	34	5 12WE	parathyroid hormone (7.97e-01	
2	51	100.0	34	5 12WE	parathyroid hormone (7.97e-01	
3	51	100.0	34	5 12WE	parathyroid hormone (7.97e-01	
4	51	100.0	35	5 12WB	parathyroid hormone (7.97e-01	
5	51	100.0	36	5 12WB	parathyroid hormone (7.97e-01	
6	51	100.0	37	5 12WB	parathyroid hormone (7.97e-01	
7	51	100.0	37	5 12WB	parathyroid hormone (7.97e-01	
8	51	100.0	115	1 PRHU	parathyroid hormone (7.97e-01	
9	51	100.0	115	2 JCA4202	parathyroid hormone (7.97e-01	
10	51	100.0	115	1 PRBG	parathyroid hormone (7.97e-01	
11	51	100.0	115	1 PRBO	parathyroid hormone (7.97e-01	
12	49	96.1	115	1 A05091	parathyroid hormone (7.97e-01	
13	46	90.2	136	2 S73520	MG441 homolog E09_crf	
14	46	90.2	201	2 C65188	hypothetical 22.3 kD	
15	45	88.2	297	2 S55085	hypothetical protein	
16	45	88.2	687	2 H64665	carbon starvation pro	
17	45	88.2	2504	2 B57788	fatty-acid synthase (1.51e+01	
18	45	88.2	2504	2 A57788	fatty-acid synthase (1.51e+01	
19	45	88.2	2505	1 XYRTFA	fatty-acid synthase (1.51e+01	
20	44	86.3	2509	2 G01880	fatty-acid synthase (1.51e+01	
21	44	86.3	227	2 S33956	ubiquitin thiolester	
22	43	84.3	2512	1 XYCHFA	fatty acid synthase (3.81e+01	
23	42	82.4	46	2 S45724	peptidylprolyl isomer	

24	42	82.4	87	2 S21218	peptidylprolyl isomer	5.98e+01
25	42	82.4	105	2 I51851	parathyroid hormone -	5.98e+01
26	42	82.4	178	5 ICYNA	cytrophilin b, chain	5.98e+01
27	42	82.4	182	5 2RKE	cytrophilin c complex	5.98e+01
28	42	82.4	182	5 2RMCC	cytrophilin c complex	5.98e+01
29	42	82.4	182	5 2RMCC	cytrophilin c complex	5.98e+01
30	42	82.4	182	5 2RMCA	Cytrophilin c complex	5.98e+01
31	42	82.4	183	2 S71547	peptidylprolyl isomer	5.98e+01
32	42	82.4	207	2 A40516	peptidylprolyl isomer	5.98e+01
33	42	82.4	208	1 CSHUB	peptidylprolyl isomer	5.98e+01
34	42	82.4	212	2 A54204	peptidylprolyl isomer	5.98e+01
35	42	82.4	212	2 A40047	peptidylprolyl isomer	5.98e+01
36	42	82.4	216	2 A56861	peptidylprolyl isomer	5.98e+01
37	42	82.4	316	2 S07569	protein H5 - slime mo	5.98e+01
38	42	82.4	541	2 A25696	yellow protein - fru1	5.98e+01
39	42	82.4	672	2 S46276	acetate--CoA ligase (5.98e+01
40	41	80.4	537	2 S67434	hypothetical protein	9.32e+01
41	41	80.4	599	2 S18612	lipoxygenase (EC 1.13	9.32e+01
42	41	80.4	632	2 S73824	MG242 homolog H21_crf	9.32e+01
43	41	80.4	864	2 S13381	lipoxygenase (EC 1.13	9.32e+01
44	41	80.4	924	2 S34926	hypothetical protein	9.32e+01
45	41	80.4	1520	2 G69634	glutamate synthase (1	9.32e+01

ALIGNMENTS

RESULT 1
 ENTRY 12WE #type complete
 TITLE parathyroid hormone (residues 4-37) - human
 ALTERNATE_NAMES HPTH(4-37)
 PDB_TITLE structure of human parathyroid hormone fragment 4-37, NMR 10
 ORGANISM #formal_name Homo sapiens #common_name man
 REFERENCE A67860
 #authors Roesch, P.; Marx, U.C.
 #submission submitted to the Brookhaven Protein Data Bank, June 1996
 #cross-references PDB:12WE
 REFERENCE TN001721
 #authors Marx, U.C.
 #book In Strukturen Verschiedener Parathormonfragmente in Loesung,
 pp.0, Bayreuth : University of Bayreuth (thesis), 1996

COMMENT Resolution: not applicable
 COMMENT Determination: NMR
 KEYWORDS hormone
 FEATURE 15-25
 SUMMARY #region helix (right hand alpha)
 #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 51; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 7.97e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 28 VHNFEVAL 34
 Qy 1 VHNFEVAL 7
 RESULT 2
 ENTRY 12WE #type complete
 TITLE parathyroid hormone 4-37 mutant N-TERMINAL SUCCINYLATED -
 ALTERNATE_NAMES n-succinyl-hPTH(4-37)
 PDB_TITLE succinyl human parathyroid hormone 4-37, NMR, 10 structures
 ORGANISM #formal_name synthetic
 REFERENCE A67743
 #authors Roesch, P.; Marx, U.C.
 #submission submitted to the Brookhaven Protein Data Bank, June 1996
 #cross-references PDB:12WE
 REFERENCE TN003319
 #authors Marx, U.C.
 #book In Strukturen Verschiedener Parathormonfragmente in Loesung,
 pp.0, Bayreuth : University of Bayreuth (thesis), 1996
 COMMENT Resolution: not applicable

COMMENT Determination: NMR
 KEYWORDS disease mutation; hormone; signal
 FEATURE
 2-9 #region helix (right hand alpha) \
 15-25 #region helix (right hand alpha) \
 SUMMARY #length 34 #molecular-weight 4128 #checksum 5508
 Query Match 100.0%; Score 51; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 7.97e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 28 VHNFEVAL 34
 QY 1 VHNFEVAL 7

Search completed: Thu Jul 30 10:57:00 1998
 Job time : 19 secs.

WIDEOR (TW)

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Search: protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:55:35 1998; MasPar time 2.08 Seconds
Tabular output not generated. 84.457 Million cell updates/sec

Title: >US-08-817-547A-25
Description: (1-7) from US08817547A.pep
Perfect Score: 51
Sequence: 1 VHNFEVAL 7

Scoring table:
PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 22.139; Variance 21.222; scale 1.043

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	51	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	8.19e-02
2	51	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	8.19e-02
3	51	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	8.19e-02
4	51	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	8.19e-02
5	49	96.1	115	1	PTHY_RAT PARATHYROID HORMONE PR	2.80e-01
6	46	90.2	136	1	Y44L_MCPN HYPOTHETICAL PROTEIN M	1.66e+00
7	46	90.2	200	1	YIGP_ECOLI HYPOTHETICAL 22.3 KD P	1.66e+00
8	45	88.2	297	1	YMY9_YEAST HYPOTHETICAL 34.0 KD P	2.95e+00
9	45	88.2	687	1	CSTA_HELPY CARBON STARAVATION PROT	2.95e+00
10	45	88.2	2504	1	FAS_HUMAN FATTY ACID SYNTHASE (E	2.95e+00
11	45	88.2	2505	1	FAS_HUMAN FATTY ACID SYNTHASE (E	2.95e+00
12	44	86.3	227	1	UBI_DRONE UBIQUITIN CARBOXYL-TER	5.18e+00
13	44	86.3	505	1	Y4XG_RHISN HYPOTHETICAL 35.5 KD P	5.18e+00
14	43	84.3	752	1	CUL1_HUMAN CULIN HOMOLOG 1 (CUL-	9.02e+00
15	43	84.3	2511	1	FAS_CHICK FATTY ACID SYNTHASE (E	1.55e+01
16	42	82.4	161	1	YCK5_EUGGR HYPOTHETICAL 18.6 KD P	1.55e+01
17	42	82.4	207	1	CYPB_CHICK PEPTIDYL-PROLYL CIS-TR	1.55e+01
18	42	82.4	208	1	CYPB_RAT PEPTIDYL-PROLYL CIS-TR	1.55e+01
19	42	82.4	208	1	CYPB_HUMAN PEPTIDYL-PROLYL CIS-TR	1.55e+01
20	42	82.4	208	1	CYPB_MOUSE PEPTIDYL-PROLYL CIS-TR	1.55e+01
21	42	82.4	208	1	CYPB_BOVIN PEPTIDYL-PROLYL CIS-TR	1.55e+01
22	42	82.4	212	1	CYPC_HUMAN PEPTIDYL-PROLYL CIS-TR	1.55e+01
23	42	82.4	212	1	CYPC_MOUSE PEPTIDYL-PROLYL CIS-TR	1.55e+01

24	42	82.4	316	1	VSH5_DICDI VEGETATIVE SPECIFIC PR	1.55e+01
25	42	82.4	541	1	YELL_DRONE YELLOW PROTEIN.	1.55e+01
26	41	80.4	537	1	AREH_SCHPO PROBABLE STEROL O-ACYL	2.64e+01
27	41	80.4	632	1	Y242_MCPN HYPOTHETICAL PROTEIN M	2.64e+01
28	41	80.4	864	1	LOXX_SOYBN SEED LIPXYGENASE (EC	2.64e+01
29	41	80.4	924	1	YB53_YEAST HYPOTHETICAL 104.5 KD	2.64e+01
30	40	78.4	216	1	Y886_CABEL HYPOTHETICAL 23.9 KD P	4.45e+01
31	40	78.4	274	1	CD1_STLFL T-CELL SURFACE GLYCOP	4.45e+01
32	40	78.4	408	1	GPT_CRIGR UDP-N-ACETYLGLUCOSAMIN	4.45e+01
33	40	78.4	408	1	GPT_CRILLO UDP-N-ACETYLGLUCOSAMIN	4.45e+01
34	40	78.4	430	1	BMP7_MOUSE BONE MORPHOGENETIC PRO	4.45e+01
35	40	78.4	444	1	BMP7_HUMAN BONE MORPHOGENETIC PRO	4.45e+01
36	40	78.4	444	1	CADB_ECOLI PROBABLE CADYERINE/LY	4.45e+01
37	40	78.4	507	1	ICK_CHICK PROTO-ONCOGENE TYROSIN	4.45e+01
38	40	78.4	578	1	YFAA_ECOLI HYPOTHETICAL 64.5 KD P	4.45e+01
39	40	78.4	607	1	UGST_SOLUI GRANULE-BOUND GLYCOSEN	4.45e+01
40	40	78.4	782	1	ZFY1_MOUSE ZINC FINGER Y-CHROMOSO	4.45e+01
41	40	78.4	783	1	ZFY2_MOUSE ZINC FINGER Y-CHROMOSO	4.45e+01
42	40	78.4	801	1	ZFY_HUMAN ZINC FINGER X-CHROMOSO	4.45e+01
43	40	78.4	805	1	ZFX_HUMAN ZINC FINGER X-CHROMOSO	4.45e+01
44	40	78.4	805	1	SEC6_YEAST EXOCYST COMPLEX COMPON	4.45e+01
45	40	78.4	847	1	ENV_HVIW2 ENVELOPE POLYPROTEIN G	4.45e+01

ALIGNMENTS

RESULT	1	PTHY_CANFA	STANDARD;	PRT;	115 AA.
AC	P52212;				
DT	01-OCT-1996 (REL. 34, CREATED)				
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)				
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).				
GN	PTH.				
OS	CANIS FAMILIARIS (DOG).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; CARNIVORA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=PARATHYROID;				
RA	MEDLINE; 95369696.				
RA	ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,				
RA	DEWILLE J.W., CAPEN C.C.,				
RL	GENE 160:241:243(1995).				
CC	-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN				
CC	BONE AND PREVENTING THEIR RENAL EXCRETION.				
DR	EMBL; U15662; G558916; -.				
DR	PROSITE; PS00335; PARATHYROID; 1.				
KW	HORMONE; SIGNAL.				
FT	SIGNAL.				
FT	PROPEP				
FT	CHAIN				
SQ	SEQUENCE	115 AA;	12957 MW;	16DEDEBC CRC32;	
Query Match					
Best Local Similarity 100.0%; Pred. No. 8.19e-02;					
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Db	62 VHNFEVAL 68				
Qy	1 VHNFEVAL 7				
RESULT 2					
ID	PTHY_BOVIN	STANDARD;	PRT;	115 AA.	
AC	P01268;				
DT	21-JUL-1986 (REL. 01, CREATED)				
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).				
GN	PTH.				
OS	BOS TAURUS (BOVINE).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				

Search completed: Thu Jul 30 10:55:41 1998
Job time : 6 secs.

```
OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 80056617.
RA KRONENBERG H.M., MCDEVITT B.E., MAJZUB J.A., NATHANS J., SHARP P.A.,
RA POTTS J.T., JR., RICH A.;
RL PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 82037785.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83105964.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
RL MOL. CELL. ENDOCRINOL. 28:411-424(1982).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84262483.
RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
RL GENE 28:319-329(1984).
RN [5]
RP SEQUENCE OF 26-115.
RX MEDLINE; 74142666.
RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T., JR.,
RA COHN D.V.;
RL PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
RN [6]
RP SEQUENCE OF 32-115.
RX MEDLINE; 71076162.
RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,
RA AURBACH G.D., POTTS J.T., JR.;
RL HOPPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).
RN [7]
RP SEQUENCE OF 32-115.
RX MEDLINE; 71063634.
RA BREWER H.B., JR., RONAN R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE; 71091568.
RA POTTS J.T., JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
RA DEPTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL; V00106; G85; -.
DR EMBL; J00023; G163641; -.
DR EMBL; J00024; G163643; -.
DR EMBL; J00024; E18249; ALT_SEQ.
DR EMBL; J00024; E18250; ALT_INIT.
DR EMBL; K01938; G163647; -.
DR EMBL; M25082; G163645; -.
DR PIR; A01534; PTBO.
DR PIR; A24949; A24949.
DR PIR; A24949; A24949.
DR PROSITE; PS00335; PARATHYROID; 1.
KW HORMONE; SIGNAL.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 PARATHYROID HORMONE.
FT CONFLICT 106 106 V->G (IN REF. 4).
SQ SEQUENCE 115 AA; 12980 MW; 673EAS5F2 CRC32;

Query Match 100.0%; Score 51; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 8,19e-02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 62 VHNFEVAL 68
Oy 1 VHNFEVAL 7
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Thu Jul 30 13:38:07 1998

US-08-817-547A-25.rspt

Page 2

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA HENNIGER R.A., JENNER K.H., HEINE H.S., KAYLER A.E., WOOD F.D.,
RA KUHAIKA F.P., PASTERNAK G.R.,
RL SUBMITTED (AUG-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- CATALYTIC ACTIVITY: ACETYL-COA + N MALONYL-COA + 2N NADPH - A
CC LONG-CHAIN FATTY ACID + (N+1) COA + N CO(2) + 2N NADP(+).
CC EMBL: U29344; G915392; -
DR PROSITE: PS00012; PHOSPHOPANTHEINE; 1.
DR PROSITE: PS00606; B. KETOACYL SYNTHASE; 1.
KM TRANSFERASE; ACYLTRANSFERASE
SQ SEQUENCE 2509 AA; 273089 MW; D1E74B76 CRC32;
Query Match 88.28; Score 45; DB 2; Length 2509;
Best Local Similarity 71.4%; Pred. No. 7.93e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
550 VHSFVSL 556
||:|:|:|
1 VHNFEVAL 7

Search completed: Thu Jul 30 10:56:24 1998
Job time : 26 secs.

WATERMAN
(TM)

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Search: protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:59:44 1998; MasPar time 2.58 Seconds
Tabular output not generated. 35.687 Million cell updates/sec

Title: >US-08-817-547A-26
Description: (1-6) from US08817547A.pep
Perfect Score: 44
Sequence: 1 HNFVAL 6

Scoring table: PAM 150
Gap 15

Searched: 124785 seqs, 1538987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 14.505; Variance 37.183; scale 0.390

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	44	100.0	38	9	R58142 [Asn21]-hPTH(1-38)-OH	4.86e+01
2	44	100.0	38	9	R58140 [Phe21]-hPTH(1-38)-OH	4.86e+01
3	44	100.0	38	9	R58129 [His19]-hPTH(1-38)-OH	4.86e+01
4	44	100.0	38	9	R58133 [Asp19]-hPTH(1-38)-OH	4.86e+01
5	44	100.0	44	26	P30015 Human parathyroid hor	4.86e+01
6	44	100.0	47	25	W21946 Fusion protein compri	4.86e+01
7	44	100.0	84	27	W25687 Human parathyroid hor	4.86e+01
8	44	100.0	84	4	R23314 Bovine parathyroid ho	4.86e+01
9	44	100.0	84	4	R23343 Bovine parathyroid ho	4.86e+01
10	44	100.0	84	4	R21199 Human parathyroid hor	4.86e+01
11	44	100.0	84	4	R23309 Bovine parathyroid ho	4.86e+01
12	44	100.0	84	4	R23492 Porcine parathyroid h	4.86e+01
13	44	100.0	84	4	R23493 Porcine parathyroid h	4.86e+01
14	44	100.0	84	4	R23276 Bovine parathyroid hor	4.86e+01
15	44	100.0	84	4	R21254 Human parathyroid hor	4.86e+01
16	44	100.0	84	4	R23384 Porcine parathyroid hor	4.86e+01
17	44	100.0	84	4	R23246 Human parathyroid hor	4.86e+01
18	44	100.0	84	4	R21175 Human parathyroid hor	4.86e+01
19	44	100.0	84	4	R21174 Human parathyroid hor	4.86e+01

20	44	100.0	84	4	R23424 Porcine parathyroid h	4.86e+01
21	44	100.0	84	4	R23383 Porcine parathyroid h	4.86e+01
22	44	100.0	84	4	R21161 Human parathyroid hor	4.86e+01
23	44	100.0	84	5	R29563 Oxidation resistant P	4.86e+01
24	44	100.0	84	4	R21241 Human parathyroid hor	4.86e+01
25	44	100.0	84	4	R21240 Human parathyroid hor	4.86e+01
26	44	100.0	84	25	W29420 Human parathyroid hor	4.86e+01
27	44	100.0	84	5	R29562 Oxidation resistant P	4.86e+01
28	44	100.0	84	5	R29561 Oxidation resistant P	4.86e+01
29	44	100.0	84	4	R23248 Human parathyroid hor	4.86e+01
30	44	100.0	84	4	R21250 Human parathyroid hor	4.86e+01
31	44	100.0	84	4	R21219 Human parathyroid hor	4.86e+01
32	44	100.0	84	4	R21187 Human parathyroid hor	4.86e+01
33	44	100.0	84	4	R23227 Human parathyroid hor	4.86e+01
34	44	100.0	84	4	R21181 Human parathyroid hor	4.86e+01
35	44	100.0	84	4	R21234 Human parathyroid hor	4.86e+01
36	44	100.0	84	4	R21238 Human parathyroid hor	4.86e+01
37	44	100.0	84	4	R23392 Porcine parathyroid h	4.86e+01
38	44	100.0	84	4	R23433 Porcine parathyroid h	4.86e+01
39	44	100.0	84	4	R23374 Bovine parathyroid hor	4.86e+01
40	44	100.0	84	4	R23240 Human parathyroid hor	4.86e+01
41	44	100.0	84	4	R23456 Porcine parathyroid ho	4.86e+01
42	44	100.0	84	4	R23363 Bovine parathyroid ho	4.86e+01
43	44	100.0	84	4	R21210 Human parathyroid hor	4.86e+01
44	44	100.0	84	4	R21211 Human parathyroid hor	4.86e+01
45	44	100.0	84	4	R23449 Porcine parathyroid h	4.86e+01

ALIGNMENTS

RESULT 1
ID R58142 standard; peptide; 38 AA.
AC R58142;
DT 20-SEP-1994 (first entry)
DE [Asn21]-hPTH(1-38)-OH.

KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
OS Synthetic.
PN GB2269176-A.
PD 02-FEB-1994.

PF 12-JUL-1993; 014384.
PR 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (BAUER) SANDOZ LTD.
PA (BAUER) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERM GES MBH.
PI Albert R. Bauer W. Breckenridge R. Cardinaux F.
PI Gombert F. Gram H. Lewis I. Ramage P. Schneider H.
PI Waelchli R. Rainer A.
DR WPI: 94-018352/03.
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 139; Page 40; 92pp; English.

CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
CC Sequence 38 AA;
SQ

Query Match 100.0%; Score 44; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.86e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 32 hnfval 37

OY 1 HNFVAL 6

RESULT 2
ID R58140 standard; peptide; 38 AA.

AC R58140;
DT 20-SEP-1994 (first entry)

DE [phe21]-hPTH(1-38)-OH;
KW Human parathyroid hormone; hPTH; variant; analogue;

KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.

OS Synthetic.

PN G52269176-A.

PD 02-FEB-1994.

PE 12-JUL-1993; 014384.

PR 15-JUL-1992; GB-015009.

PR 18-DEC-1992; GB-026415.

PR 23-DEC-1992; GB-026859.

23-DEC-1992; GB-026861.

28-JAN-1993; GB-001691.

28-JAN-1993; GB-001692.

14-APR-1993; GB-007673.

19-APR-1993; GB-008033.

PR (SANO) SANDOZ LTD.

PA (BAVE/) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERM GES MBH.

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;

PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

PI Waelchli R, Rainer A;

PI WPI: 94-018352/03.

DR New active para-thyroid hormone variants - used for treating or

PT Preventing osteoporosis etc.

PS Example 137; Page 40; 92pp; English.

CC This peptide is an example of a highly generic formula covering

CC parathyroid hormone variants useful for treating or preventing bone

CC conditions associated with calcium depletion/resorption, in cases

CC where calcium fixation is required (esp. osteoporosis) or to treat

CC hypoparathyroidism.

SQ Sequence 38 AA;

Query Match 100.0%; Score 44; DB 9; Length 38;

Best Local Similarity 100.0%; Pred. No. 4.86e+01; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0;

Db 32 hnfval 37

1 HNFVAL 6

Search completed: Thu Jul 30 10:59:59 1998
Job time : 15 secs.

WATERMAN (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:59:09 1998; Maspar time 3.02 Seconds
Tabular output not generated. 72.657 Million cell updates/sec

Title: >US-08-817-547A-26
Description: (1-6) from US08817547A.pep
Perfect Score: 44
Sequence: 1 HNFVAL 6

Scoring table: PAM 150
Gap 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir56

1:pir1 2:pir2 3:pir3 4:pir4 5:nr13d

Statistics: Mean 20.121; Variance 22.615; scale 0.890

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	44	100.0	34	5 12WE	parathyroid hormone (6.34e+00	
2	44	100.0	34	5 12WG	parathyroid hormone 4 6.34e+00	
3	44	100.0	34	5 12WF	parathyroid hormone 4 6.34e+00	
4	44	100.0	35	5 12WD	parathyroid hormone (6.34e+00	
5	44	100.0	36	5 12WB	parathyroid hormone (6.34e+00	
6	44	100.0	37	5 12WH	parathyroid hormone (6.34e+00	
7	44	100.0	37	5 12WC	parathyroid hormone (6.34e+00	
8	44	100.0	115	1 PTHU	parathyroid hormone P 6.34e+00	
9	44	100.0	115	1 JCA4202	parathyroid hormone P 6.34e+00	
10	44	100.0	115	1 PRPG	parathyroid hormone P 6.34e+00	
11	44	100.0	115	1 PRBO	parathyroid hormone P 6.34e+00	
12	42	95.5	105	2 F51851	parathyroid hormone P 1.77e+01	
13	42	95.5	115	2 A05091	parathyroid hormone P 1.77e+01	
14	42	95.5	541	2 A25696	yellow protein - fru1 1.77e+01	
15	40	90.9	498	2 A34996	hypothetical protein 4.76e+01	
16	40	90.9	406	2 A37813	UDP-N-acetylglucosam 4.76e+01	
17	40	90.9	410	2 S24326	UDP-N-acetylglucosam 4.76e+01	
18	40	90.9	430	2 JQ1184	osteogenic protein 1 4.76e+01	
19	40	90.9	431	1 BMH07	bone morphogenetic pr 4.76e+01	
20	40	90.9	507	2 A39939	protein-tyrosine kina 4.76e+01	
21	40	90.9	578	2 D64993	yfiaa protein - Escher 4.76e+01	
22	40	90.9	581	2 G70189	threonine--trna ligas 4.76e+01	
23	40	90.9	924	2 S34926	hypothetical protein 4.76e+01	

24	40	90.9	997	2 A60776	230k bullous pemphig	4.76e+01
25	39	88.6	136	2 S73520	Mg441 homolog E09.orf	7.71e+01
26	39	88.6	201	2 C65188	hypothetical 22.3 kd	7.71e+01
27	39	88.6	208	2 JC5638	pH-sensing regulatory	7.71e+01
28	39	88.6	212	2 S39965	hypothetical protein	7.71e+01
29	39	88.6	227	2 S39965	ubiquitin thiolstera	7.71e+01
30	39	88.6	259	2 D69598	maturatin of the cut	7.71e+01
31	39	88.6	504	2 I40811	urotoporphyrinogen-III	7.71e+01
32	39	88.6	707	2 S43297	oligopeptide transpor	7.71e+01
33	39	88.6	708	2 A56163	peptide transport pro	7.71e+01
34	39	88.6	710	2 S68161	oligopeptide transpor	7.71e+01
35	39	88.6	710	2 S72497	oligopeptide transpor	7.71e+01
36	39	88.6	798	2 JN0878	100k protein - fowl a	7.71e+01
37	39	88.6	885	2 S67660	hypothetical protein	7.71e+01
38	38	86.4	388	2 S04110	integrinase - streptom	1.24e+02
39	38	86.4	397	2 G69287	hypothetical protein	1.24e+02
40	38	86.4	409	2 A42363	peptidase T - Salmo	1.24e+02
41	38	86.4	508	2 G69593	endo-1,4-beta-glucana	1.24e+02
42	38	86.4	582	2 A49626	transregulatory prote	1.24e+02
43	38	86.4	604	2 S66993	hypothetical protein	1.24e+02
44	38	86.4	711	2 E69121	conserved hypotherica	1.24e+02
45	38	86.4	2504	2 A57788	fatty-acid synthase (1.24e+02

ALIGNMENTS

RESULT	1	12WE	#type complete
ENTRY			parathyroid hormone (residues 4-37) - human
TITLE			HPTH(4-37)
ALTERNATE_NAMES			structure of human parathyroid hormone fragment 4-37, NMR 10
PDB_TITLE			structures
ORGANISM			#formal_name Homo sapiens #common_name man
REFERENCE			A67860
#authors			Roesch, P.; Marx, U.C.
#submission			submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references			PDB:12WE
REFERENCE			TN001721
#authors			Marx, U.C.
#book			In Strukturen Verschiedener Parathormonfragmente In Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996
COMMENT			Resolution: not applicable
KEYWORDS			Determination: NMR
FEATURE			hormone
SUMMARY			#region helix (right hand alpha) #length 34 #molecular-weight 4128 #checksum 5508
Query Match			100.0%; Score 44; DB 5; Length 34;
Best Local Similarity			100.0%; Pred. No. 6.34e+00;
Matches			6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	29	HNFVAL	34
Qy	1	HNFVAL	6
RESULT	2	12WG	#type complete
ENTRY			parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -
TITLE			synthetic
ALTERNATE_NAMES			n-succinyl-hPTH(4-37)
PDB_TITLE			succinyl human parathyroid hormone 4-37, NMR, 10 structures
ORGANISM			#formal_name synthetic
REFERENCE			A67743
#authors			Roesch, P.; Marx, U.C.
#submission			submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references			PDB:12WG
REFERENCE			TN003319
#authors			Marx, U.C.
#book			In Strukturen Verschiedener Parathormonfragmente In Loesung, pp.0, Bayreuth : University of Bayreuth (thesis), 1996
COMMENT			Resolution: not applicable

COMMENT Determination: NMR
 KEYWORDS disease mutation; hormone; signal
 FEATURE
 2-9 #region helix (right hand alpha) \
 15-25 #region helix (right hand alpha) \
 SUMMARY #length 34 #molecular-weight 4128 #checksum 5508
 Query Match 100.0%; Score 44; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 6.34e+00;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 29 HNFVAL 34
 QY 1 HNFVAL 6

Search completed: Thu Jul 30 10:59:26 1998
 Job time : 17 secs.

M0505000
(TW)

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Mparch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:57:48 1998; Maspar time 2.03 Seconds
Tabular output not generated. 74.131 Million cell updates/sec

Title: >US-08-817-547A-26
Description: (1-6) from US08817547A.pep
Perfect Score: 44
Sequence: 1 HNFVAL 6

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swlssl

Statistics: Mean 21.045; Variance 18.682; scale 1.127

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	44	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	1.12e+00
2	44	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	1.12e+00
3	44	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	1.12e+00
4	44	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	1.12e+00
5	42	95.5	115	1	PTHY_RAT PARATHYROID HORMONE PR	3.84e+00
6	42	95.5	115	1	PTHY_MOUSE PARATHYROID HORMONE PR	3.84e+00
7	40	90.9	408	1	YELL_DROME YELLOW PROTEIN.	1.26e+01
8	40	90.9	408	1	GPT_CRIGO UDP-N-ACETYLGLUCOSAMIN	1.26e+01
9	40	90.9	408	1	GPT_MOUSE UDP-N-ACETYLGLUCOSAMIN	1.26e+01
10	40	90.9	430	1	BMP7_MOUSE BONE MORPHOGENETIC PRO	1.26e+01
11	40	90.9	431	1	BMP7_HUMAN BONE MORPHOGENETIC PRO	1.26e+01
12	40	90.9	507	1	LCK_CHICK PROTO-ONCOGENE TYROSIN	1.26e+01
13	40	90.9	578	1	YFSA_ECOLI HYPOTHETICAL 64.5 KD P	1.26e+01
14	40	90.9	924	1	YFSA_YEAST HYPOTHETICAL 104.5 KD	1.26e+01
15	39	88.6	104	1	CGEE_BACSU CGEE PROTEIN (FRAGMENT	2.23e+01
16	39	88.6	136	1	Y441_MYCPN HYPOTHETICAL 22.3 KD P	2.23e+01
17	39	88.6	200	1	YIGP_ECOLI HYPOTHETICAL 22.3 KD P	2.23e+01
18	39	88.6	227	1	UBI_DROME UBIQUITIN CARBOXYL-TER	2.23e+01
19	39	88.6	504	1	HEW4_CLOUD UROPODEPRYRIN-III C-MET	2.23e+01
20	39	88.6	707	1	PEP1_RABIT OLIGOPEPTIDE TRANSPORT	2.23e+01
21	39	88.6	708	1	PEP1_HUMAN OLIGOPEPTIDE TRANSPORT	2.23e+01
22	39	88.6	710	1	PEP1_RAT OLIGOPEPTIDE TRANSPORT	2.23e+01
23	39	88.6	798	1	L100_ADEGX LATE 100 KD PROTEIN.	2.23e+01

24	39	88.6	984	1	L100_ADEGX LATE 100 KD PROTEIN.	2.23e+01
25	38	86.4	249	1	UL07_HSV60 PROTEIN U75.	3.91e+01
26	38	86.4	249	1	UL07_HSV62 PROTEIN U75.	3.91e+01
27	38	86.4	259	1	UDP_HAELN URIDINE PHOSPHORYLASE	3.91e+01
28	38	86.4	289	1	ROB_ECOLI RIGHT ORIGIN-BINDING P	3.91e+01
29	38	86.4	297	1	YMY9_YEAST HYPOTHETICAL 34.0 KD P	3.91e+01
30	38	86.4	388	1	INTR_STRAM INDEGRASE.	3.91e+01
31	38	86.4	408	1	PEPT_ECOLI PEPTIDASE T (EC 3.4.11	3.91e+01
32	38	86.4	409	1	PEPT_SALTY PEPTIDASE T (EC 3.4.11	3.91e+01
33	38	86.4	499	1	GUN2_BACSU ENDOGLUCANASE PRECURSO	3.91e+01
34	38	86.4	499	1	GUN1_BACSU ENDOGLUCANASE PRECURSO	3.91e+01
35	38	86.4	536	1	YB36_YEAST HYPOTHETICAL 60.5 KD P	3.91e+01
36	38	86.4	541	1	DETI_ARATH LIGHT-MEDIATED DEVELOP	3.91e+01
37	38	86.4	560	1	TATR_NPVCE TRANS-ACTIVATING TRANS	3.91e+01
38	38	86.4	560	1	TATR_NPVOP TRANS-ACTIVATING TRANS	3.91e+01
39	38	86.4	582	1	TATR_NPVAC TRANS-ACTIVATING TRANS	3.91e+01
40	38	86.4	587	1	TATR_NPVAM TRANS-ACTIVATING TRANS	3.91e+01
41	38	86.4	591	1	LAC1_CRYPA LACCASE PRECURSOR (EC	3.91e+01
42	38	86.4	687	1	CSTA_HELPY CARBON STARVATION PROT	3.91e+01
43	38	86.4	790	1	TNP3_HUMAN TUMOR NECROSIS FACTOR,	3.91e+01
44	38	86.4	790	1	FAS_HUMAN FATTY ACID SYNTHASE (E	3.91e+01
45	38	86.4	2505	1	FAS_RAT FATTY ACID SYNTHASE (E	3.91e+01

ALIGNMENTS

RESULT	1	STANDARD;	PRT;	115 AA.
ID	PTHY_CANFA			
AC	P52212;			
DT	01-OCT-1996 (REL. 34, CREATED)			
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).			
GN	PTH.			
OS	CANIS FAMILIARIS (DOG).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; CARNIVORA.			
NC	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PARATHYROID;			
RX	MEDLINE: 95369696.			
RA	ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,			
RL	DEVILLE J.W., CAPEN C.C.;			
CC	G-1 FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN			
CC	BONE AND PREVENTING THEIR RENAL EXCRETION.			
DR	EMBL: U15662; G558916; "			
CC	BONE AND PREVENTING THEIR RENAL EXCRETION.			
DR	PROTINE; PS00335; PARATHYROID: 1.			
KW	HORMONE; SIGNAL.			
FT	SIGNAL			
FT	PROPEP			
FT	CHAIN			
SO	SEQUENCE			
Query Match	100.0%;	Score 44;	DB 1;	Length 115;
Best Local Similarity	100.0%;	Pred. No. 1.12e+00;		
Matches	6;	Conservative	0;	Mismatches 0;
Indels			0;	Gaps 0;
DB	63 HNFVAL 68			
QY	1 HNFVAL 6			
RESULT	2	STANDARD;	PRT;	115 AA.
ID	PTHY_BOVIN			
AC	P01268;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).			
GN	PTH.			
OS	BOS TAUROS (BOVINE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			

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Msrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:58:11 1998; Maspar time 3.65 Seconds
69.158 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-26
Description: (1-6) from US08817547A.pep
Percent Score: 44
Sequence: 1 HNFVAL 6

Scoring table: PAM 150
Gap 15

Searched: 140542 segs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptemb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 20.282; Variance 20.253; scale 1.001

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	42	95.5	105	10	063473	PARATHYROID HORMONE (F	1.01e+01
2	42	95.5	568	3	002437	YELLOW	1.01e+01
3	42	95.5	2408	2	092566	MELOBLAST KIAA0279 (F	1.01e+01
4	41	93.2	1149	3	023315	ZC434.5.	1.76e+01
5	41	93.2	1774	3	093636	F2966.3B.	1.76e+01
6	41	93.2	1918	3	093637	F2966.3A.	1.76e+01
7	40	90.9	296	9	P76472	FROM BASES 2360084 TO	3.04e+01
8	40	90.9	400	2	015216	GLCNAC-1-P TRANSFERASE	3.04e+01
9	40	90.9	562	9	P76923	SIMILAR TO.	3.04e+01
10	40	90.9	635	3	018199	Y48E1B.5.	3.04e+01
11	40	90.9	747	3	020046	COSMID F35D2.	3.04e+01
12	39	88.6	154	3	016894	BAHAMA HEMOLYMPH POLYP	5.18e+01
13	39	88.6	208	2	014496	PH-SENSING REGULATOR	5.18e+01
14	39	88.6	208	9	033707	PUTATIVE EPIMERASE.	5.18e+01
15	39	88.6	212	9	054198	DNA SEQUENCE FOR ORF'S	5.18e+01
16	39	88.6	554	3	009995	PUTATIVE POLY(A) POLYM	5.18e+01
17	39	88.6	635	1	013781	HYPOTHETICAL 71.4 KD P	5.18e+01
18	39	88.6	726	9	032971	ABC-TYPE TRANSPORTER.	5.18e+01
19	39	88.6	805	3	013005	SIMILAR TO F-SPONIN.	5.18e+01
20	39	88.6	885	1	007533	CHROMOSOME IV READING	5.18e+01

RESULT	ID	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	063473	95.5	105	10	063473	PARATHYROID HORMONE (F	1.01e+01	
2	063473	95.5	568	3	002437	YELLOW	1.01e+01	
3	063473	95.5	2408	2	092566	MELOBLAST KIAA0279 (F	1.01e+01	
4	063473	95.5	1149	3	023315	ZC434.5.	1.76e+01	
5	063473	95.5	1774	3	093636	F2966.3B.	1.76e+01	
6	063473	95.5	1918	3	093637	F2966.3A.	1.76e+01	
7	063473	95.5	296	9	P76472	FROM BASES 2360084 TO	3.04e+01	
8	063473	95.5	400	2	015216	GLCNAC-1-P TRANSFERASE	3.04e+01	
9	063473	95.5	562	9	P76923	SIMILAR TO.	3.04e+01	
10	063473	95.5	635	3	018199	Y48E1B.5.	3.04e+01	
11	063473	95.5	747	3	020046	COSMID F35D2.	3.04e+01	
12	063473	95.5	154	3	016894	BAHAMA HEMOLYMPH POLYP	5.18e+01	
13	063473	95.5	208	2	014496	PH-SENSING REGULATOR	5.18e+01	
14	063473	95.5	208	9	033707	PUTATIVE EPIMERASE.	5.18e+01	
15	063473	95.5	212	9	054198	DNA SEQUENCE FOR ORF'S	5.18e+01	
16	063473	95.5	554	3	009995	PUTATIVE POLY(A) POLYM	5.18e+01	
17	063473	95.5	635	1	013781	HYPOTHETICAL 71.4 KD P	5.18e+01	
18	063473	95.5	726	9	032971	ABC-TYPE TRANSPORTER.	5.18e+01	
19	063473	95.5	805	3	013005	SIMILAR TO F-SPONIN.	5.18e+01	
20	063473	95.5	885	1	007533	CHROMOSOME IV READING	5.18e+01	

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	063473	95.5	105	10	063473	PARATHYROID HORMONE (F	1.01e+01	
2	063473	95.5	568	3	002437	YELLOW	1.01e+01	
3	063473	95.5	2408	2	092566	MELOBLAST KIAA0279 (F	1.01e+01	
4	063473	95.5	1149	3	023315	ZC434.5.	1.76e+01	
5	063473	95.5	1774	3	093636	F2966.3B.	1.76e+01	
6	063473	95.5	1918	3	093637	F2966.3A.	1.76e+01	
7	063473	95.5	296	9	P76472	FROM BASES 2360084 TO	3.04e+01	
8	063473	95.5	400	2	015216	GLCNAC-1-P TRANSFERASE	3.04e+01	
9	063473	95.5	562	9	P76923	SIMILAR TO.	3.04e+01	
10	063473	95.5	635	3	018199	Y48E1B.5.	3.04e+01	
11	063473	95.5	747	3	020046	COSMID F35D2.	3.04e+01	
12	063473	95.5	154	3	016894	BAHAMA HEMOLYMPH POLYP	5.18e+01	
13	063473	95.5	208	2	014496	PH-SENSING REGULATOR	5.18e+01	
14	063473	95.5	208	9	033707	PUTATIVE EPIMERASE.	5.18e+01	
15	063473	95.5	212	9	054198	DNA SEQUENCE FOR ORF'S	5.18e+01	
16	063473	95.5	554	3	009995	PUTATIVE POLY(A) POLYM	5.18e+01	
17	063473	95.5	635	1	013781	HYPOTHETICAL 71.4 KD P	5.18e+01	
18	063473	95.5	726	9	032971	ABC-TYPE TRANSPORTER.	5.18e+01	
19	063473	95.5	805	3	013005	SIMILAR TO F-SPONIN.	5.18e+01	
20	063473	95.5	885	1	007533	CHROMOSOME IV READING	5.18e+01	

RP SEQUENCE FROM N.A.
 RA SAGARRA C.; TO EMBL/GENBANK/DBJ DATA BANKS.
 RL SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; Y13909; E324295; -
 DR FLYBASE: FBgn0015179; DsubV.
 SQ SEQUENCE 568 AA; 62589 MW; 6F52A641 CRC32;

Query Match 95.5%; Score 42; DB 3; Length 568;
 Best Local Similarity 83.3%; Pred. No. 1.01e+01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 301 HDEFVAL 306
 Oy 1 HDEFVAL 6

Search completed: Thu Jul 30 10:58:51 1998
 Job time : 40 secs.

M E S S E G E (TM)

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MPsrch.p protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:02:08 1998; Maspar time 2.54 Seconds
30.164 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-27
Description: (1-5) from US08817547A.pep
Perfect Score: 35
Sequence: 1 NEFVAL 5

Scoring table: PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 13.768; Variance 32.782; scale 0.420

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	35	100.0	38	9	R58019 N-alpha-methyl[Ala1]	3.36e+02
2	35	100.0	38	9	R58126 [Ala19]-hPTH(1-38)-OH	3.36e+02
3	35	100.0	38	9	R58129 [His19]-hPTH(1-38)-OH	3.36e+02
4	35	100.0	38	9	R58133 [Asp19]-hPTH(1-38)-OH	3.36e+02
5	35	100.0	44	26	P30015 Human parathyroid hor	3.36e+02
6	35	100.0	47	25	W21946 Fusion protein compri	3.36e+02
7	35	100.0	84	27	W25687 Human parathyroid hor	3.36e+02
8	35	100.0	84	4	R23524 Human parathyroid hor	3.36e+02
9	35	100.0	84	4	R23227 Human parathyroid hor	3.36e+02
10	35	100.0	84	4	R21199 Human parathyroid hor	3.36e+02
11	35	100.0	84	4	R23309 Bovine parathyroid ho	3.36e+02
12	35	100.0	84	4	R23396 Porcine parathyroid h	3.36e+02
13	35	100.0	84	4	R23435 Porcine parathyroid h	3.36e+02
14	35	100.0	84	4	R21255 Human parathyroid hor	3.36e+02
15	35	100.0	84	4	R21254 Human parathyroid hor	3.36e+02
16	35	100.0	84	4	R21179 Human parathyroid hor	3.36e+02
17	35	100.0	84	4	R23332 Bovine parathyroid hor	3.36e+02
18	35	100.0	84	4	R23501 Porcine parathyroid h	3.36e+02
19	35	100.0	84	4	R23500 Porcine parathyroid h	3.36e+02

20	35	100.0	84	4	R21161 Human parathyroid hor	3.36e+02
21	35	100.0	84	4	R21160 Human parathyroid hor	3.36e+02
22	35	100.0	84	25	W29420 Human parathyroid hor	3.36e+02
23	35	100.0	84	5	R29562 Oxidation resistant l	3.36e+02
24	35	100.0	84	5	R29561 Oxidation resistant p	3.36e+02
25	35	100.0	84	4	R23478 Porcine parathyroid h	3.36e+02
26	35	100.0	84	4	R23346 Bovine parathyroid ho	3.36e+02
27	35	100.0	84	4	R21219 Human parathyroid hor	3.36e+02
28	35	100.0	84	4	R23353 Bovine parathyroid ho	3.36e+02
29	35	100.0	84	4	R23379 Bovine parathyroid ho	3.36e+02
30	35	100.0	84	4	R23260 Bovine parathyroid ho	3.36e+02
31	35	100.0	84	4	R23336 Bovine parathyroid ho	3.36e+02
32	35	100.0	84	4	R23392 Porcine parathyroid h	3.36e+02
33	35	100.0	84	4	R23433 Porcine parathyroid h	3.36e+02
34	35	100.0	84	4	R23384 Porcine parathyroid h	3.36e+02
35	35	100.0	84	4	R23246 Human parathyroid hor	3.36e+02
36	35	100.0	84	4	R21175 Human parathyroid hor	3.36e+02
37	35	100.0	84	4	R21174 Human parathyroid hor	3.36e+02
38	35	100.0	84	4	R21210 Human parathyroid hor	3.36e+02
39	35	100.0	84	4	R21211 Human parathyroid hor	3.36e+02
40	35	100.0	84	5	R29563 Oxidation resistant p	3.36e+02
41	35	100.0	115	13	R75693 Human prepro-PTH	3.36e+02
42	35	100.0	115	25	W23060 Mouse beta 2 integrin	3.36e+02
43	35	100.0	115	14	R78167 Mouse alpha-d subunit	3.36e+02
44	35	100.0	116	15	W23061 Mouse beta 2 integrin	3.36e+02
45	35	100.0	116	14	R78168 Mouse alpha-d subunit	3.36e+02

ALIGNMENTS

RESULT 1
ID R58019 standard; peptide; 38 AA.
AC R58019; 20-SEP-1994 (first entry)
DE N-alpha-methyl[Ala1] parathyroid hormone(1-38).
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_site 1 /note="N-alpha-methyl-Ala replaces wild-type
Ser residue at position 1"
FT Ser residue at position 1"
FN
PD 02-FEB-1994.
PD 12-JUL-1993; 014384.
PF 15-JUL-1992; GB-015009.
PR 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (SANO) SANDOZ LTD.
PA (BAUER) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F,
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H,
PI Maechli R, Rainer A;
DR WPI: 94-018352/03.
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 4; Page 34; 92pp; English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption. In cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 38 AA;

Query Match 100.0%; Score 35; DB 9; Length 38;

Best Local Similarity 100.0%; Pred. No. 3.36e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 33 nFVAL 37
| | | | |
QY 1 NFWAL 5

RESULT 2
ID R58126 standard; peptide; 38 AA.
AC R58126;
DT 20-SEP-1994 (first entry)
DE [Ala19]-hPTH(1-38)-OH.
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
PN GB2269176-A.
PD 02-FEB-1994.
PT 12-JUL-1993; 014384.
PR 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (SANO) SANDOZ LTD.
PA (BAUE/) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F,
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Maelchli R, Rainer A.
DR WPI: 94-018352/03.
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 123; Page 39; 92pp; English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 38 AA;

Query Match 100.0%; Score 35; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.36e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
33 nFVAL 37
| | | | |
QY 1 NFWAL 5

Search completed: Thu Jul 30 11:02:23 1998
Job time : 15 secs.

W E S E L F (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:01:26 1998; MasPar time 3.08 Seconds
Tabular output not generated. 59.234 Million cell updates/sec

Title: >US-08-817-547A-27
Description: (1-5) from US08817547A.pep
Perfect Score: 35
Sequence: 1 NFVAL 5

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r56
1:p1r1 2:p1r2 3:p1r3 4:p1r4 5:nr13d

Statistics: Mean 19.157; Variance 19.754; scale 0.970

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	35	100.0	34	5	1ZWF parathyroid hormone 4	1.85e+02
2	35	100.0	34	5	1ZMG parathyroid hormone 4	1.85e+02
3	35	100.0	34	5	1ZWE parathyroid hormone 4	1.85e+02
4	35	100.0	35	5	1ZMD parathyroid hormone 4	1.85e+02
5	35	100.0	36	5	1ZMB parathyroid hormone 4	1.85e+02
6	35	100.0	37	5	1ZMC parathyroid hormone 4	1.85e+02
7	35	100.0	37	5	1ZMC parathyroid hormone 4	1.85e+02
8	35	100.0	46	2	S45724 parathyroid hormone 4	1.85e+02
9	35	100.0	87	2	S21218 parathyroid hormone 4	1.85e+02
10	35	100.0	115	1	PTBO parathyroid hormone 4	1.85e+02
11	35	100.0	115	2	JC4202 parathyroid hormone 4	1.85e+02
12	35	100.0	115	1	PTHU parathyroid hormone 4	1.85e+02
13	35	100.0	115	1	PTHU parathyroid hormone 4	1.85e+02
14	35	100.0	140	2	A69445 parathyroid hormone 4	1.85e+02
15	35	100.0	178	5	1CYNA cyclophilin b, chain	1.85e+02
16	35	100.0	182	5	2RMCE cyclophilin c complex	1.85e+02
17	35	100.0	182	5	2RMCG cyclophilin c complex	1.85e+02
18	35	100.0	182	5	2RMCC cyclophilin c complex	1.85e+02
19	35	100.0	182	5	2RMCA cyclophilin c complex	1.85e+02
20	35	100.0	183	2	S71547 peptidylprolyl isomer	1.85e+02
21	35	100.0	201	2	C65188 hypothetical 22.3 kD	1.85e+02
22	35	100.0	207	2	A40516 peptidylprolyl isomer	1.85e+02
23	35	100.0	208	1	CSHUB peptidylprolyl isomer	1.85e+02

24	35	100.0	212	2	A40047	peptidylprolyl isomer	1.85e+02
25	35	100.0	212	2	A54204	peptidylprolyl isomer	1.85e+02
26	35	100.0	215	2	S75497	hypothetical protein	1.85e+02
27	35	100.0	216	2	A56861	peptidylprolyl isomer	1.85e+02
28	35	100.0	292	2	G69417	conserved hypothetical	1.85e+02
29	35	100.0	345	2	S73498	MG456 homolog K05_orf	1.85e+02
30	35	100.0	352	2	JT0321	photosystem II protein	1.85e+02
31	35	100.0	362	2	JQ1602	replication protein B	1.85e+02
32	35	100.0	448	1	B26981	C4-dicarboxylate tran	1.85e+02
33	35	100.0	460	1	C33586	ADP-heptose synthase	1.85e+02
34	35	100.0	476	2	C64127	hypothetical protein	1.85e+02
35	35	100.0	533	2	S74401	probable membrane pro	1.85e+02
36	35	100.0	538	2	S64842	equine arteritis virus	1.85e+02
37	35	100.0	540	2	B40901	acid protein - Provid	1.85e+02
38	35	100.0	588	2	S70900	mdlb protein - Escher	1.85e+02
39	35	100.0	593	2	A64775	SEC6 protein - yeast	1.85e+02
40	35	100.0	805	2	S48411	hypothetical protein	1.85e+02
41	35	100.0	879	2	S73757	hypothetical protein	1.85e+02
42	35	100.0	1139	2	S28277	mdl protein - Escheri	1.85e+02
43	35	100.0	1143	2	I84547	transcription factor	1.85e+02
44	35	100.0	1160	2	A46423	protein disulfide iso	4.83e+02
45	33	94.3	517	2	A44483		

ALIGNMENTS

RESULT 1
ENTRY 1
TITLE 1ZWF #type complete
PDB_TITLE parathyroid hormone 4 37 mutant N-TERMINAL ACETYLATED -
ALTERNATE_NAMES n-acetyl-hpnh(4-37)
STRUCTURE structure of n-terminal acetylated human parathyroid hormone,
NMR, 10 structures
ORGANISM #formal_name synthetic
#authors Roesch, P.; Marx, U.C.
#submission submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references PDB:1ZWF
REFERENCE JN003318
#authors Marx, U.C.
#book in Strukturen Verschiedener Parathormonfragmente in Loesung,
pp.0, Bayreuth: Universitaet Bayreuth (Thesis), 1996
COMMENT Resolution: not applicable
KEYWORDS Determination: NMR
FEATURES
3-6
14-27 #region helix (right hand alpha)\
SUMMARY #length 34 #molecular-weight 4128 #checksum 5508
Query Match 100.0%; Score 35; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.85e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 30 NFVAL 34
QY 1 NFVAL 5
RESULT 2
ENTRY 1ZMG #type complete
PDB_TITLE parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -
ALTERNATE_NAMES n-succinyl-hpnh(4-37)
STRUCTURE succinyl human parathyroid hormone 4-37, NMR, 10 structures
ORGANISM #formal_name synthetic
#authors Roesch, P.; Marx, U.C.
#submission submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references PDB:1ZMG
REFERENCE JN003319
#authors Marx, U.C.
#book in Strukturen Verschiedener Parathormonfragmente in Loesung,

COMMENT PP.0, Bayreuth : University of Bayreuth (Thesis), 1996
 RESOLUTION: not applicable
 DETERMINATION: NMR
 KEYWORDS disease mutation; hormone; signal
 FEATURE 2-9
 SUMMARY 15-25
 #region helix (right hand alpha) \
 #region helix (right hand alpha) \
 #length 34 #molecular-weight 4128 #checksum 5508
 Query Match 100.0%; Score 35; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.85e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 30 NEVAL 34
 QY 1 NEVAL 5
 Search completed: Thu Jul 30 11:01:50 1998
 CPU time : 24 secs.

RP REVISIONS.
 RX MEDLINE: 75146516.
 RA KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL BIOCHEMISTRY 14:1842-1847(1975).
 RN [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 75059220.
 RA TREGEAR G.W., VAN RIJNSCHOTEN J., GREEN E., NIALL H.D.,
 KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL HOPE-SEYLER S.Z. PHYSIOL. CHEM. 355:415-421(1974).
 RN [9]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 73227467.
 RA ANDREATA R.H., HARTMANN A., JOEHL A., KAMBER B., MAIER R.,
 RINKER B., RITTEL W., SIEBER P.;
 RL HELV. CHIM. ACTA 56:470-473(1973).
 RN [10]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE: 91299748.
 RA KLAUS W., DIECKMANN T., WRAY V., SCHOMBURG D., WINGENDER E., MAYER H.;
 RL BIOCHEMISTRY 30:6936-6942(1991).
 RN [11]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE: 93345318.
 RA BARDEN J.A., CUTHBERTSON R.M.;
 RL EUR. J. BIOCHEM. 215:315-321(1993).
 RN [12]
 RP STRUCTURE BY NMR OF 32-68.
 RX MEDLINE: 95318084.
 RA MARX U.C., AUSTERMANN S., BAYER P., ADERHANN K., ECHART A.,
 STICHT H., WALTER S., SCHMID F.-X., JAENICKE R., FORSSMANN W.-G.,
 ROESCH P.;
 RL J. BIOL. CHEM. 270:15194-15202(1995).
 RN [13]
 RP VARIANT ARG-18.
 RX MEDLINE: 91009811.
 RA ARNOED A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,
 KRONENBERG H.M.;
 RL J. CLIN. INVEST. 86:1084-1087(1990).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
 HYPOPARATHYROIDISM (PIH).
 DR EMBL: J00301: G190704; -.
 DR EMBL: V00597: G37144; -.
 DR EMBL: A29146: E186700; -.
 DR PIR: A01536; PTHU
 DR PIR: A01539; A19338
 DR PDB: 1HPH: 10-JUL-95.
 DR PDB: 1HTH: 15-OCT-97.
 DR PDB: 1ZMA: 12-MAR-97.
 DR PDB: 1ZMB: 12-MAR-97.
 DR PDB: 1ZWC: 12-MAR-97.
 DR PDB: 1ZWD: 12-MAR-97.
 DR PDB: 1ZWE: 12-MAR-97.
 DR PDB: 1ZWF: 16-JUN-97.
 DR PDB: 1ZWG: 16-JUN-97.
 DR MIM: 146200; -.
 DR MIM: 168450; -.
 DR PROSITE: PS00335; PARATHYROID: 1.
 KW HORMONE; SIGNAL; DISEASE MUTATION; 3D-STRUCTURE.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT VARIANT 18 18
 FT CONFLICT 107 107
 FT SEQUENCE 115 AA: 12861 MM; 243E87C7 CRC32;
 SQ
 Query Match 100.0%; Score 35; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 6.41e+01;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 64 NEVAL 68
 QY 1 NEVAL 5
 ID RESULT 2
 AC P01268; STANDARD; PRT; 115 AA.
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
 GN BOS TAURUS (BOVINE).
 OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; ARTIODACTYLA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 80056617.
 RA KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
 RA POTTS J.T. JR., RICH A.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 82037785.
 RA WEAYER C.A., GORDON D.F., KEMPER B.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 83105964.
 RA WEAYER C.A., GORDON D.F., KEMPER B.;
 RL MOL. CELL. ENDOCRINOL. 28:411-424(1982).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 84262483.
 RA WEAYER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
 RL GENE 28:319-329(1984).
 RN [5]
 RP SEQUENCE OF 26-115.
 RX MEDLINE: 74142666.
 RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,
 RA COHN D.V.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
 RN [6]
 RP SEQUENCE OF 32-115.
 RX MEDLINE: 71076162.
 RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,
 RA AUBRACH G.D., POTTS J.T. JR.;
 RL HOPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).
 RN [7]
 RP SEQUENCE OF 32-115.
 RX MEDLINE: 71063634.
 RA BREMER H.B. JR., ROMAN R.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
 RN [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 71091588.
 RA POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
 RA DEFTOS L.J., DAWSON B.F., HOGAN M.L., AUBRACH G.D.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971)
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC EMBL: J00023: G163641; -.
 DR EMBL: J00023: G163643; -.
 DR EMBL: J00024: E18245; ALT_SEQ.
 DR EMBL: J00024: E18250; ALT_INIT.
 DR EMBL: K01938: G163647; -.
 DR EMBL: M25082: G163645; -.
 DR PIR: A01534; PTHO.
 DR PIR: A24949: A24949.
 DR PROSITE: PS00335; PARATHYROID: 1.
 KW HORMONE; SIGNAL.

FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT CONFLICT 106 106
 SQ SEQUENCE 115 AA; 12980 MM; 673EA5F2 CRC32;
 PARATHYROID HORMONE.
 V -> G (IN REF. 4).

Query Match 100.0%; Score 35; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 6.41e+01;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 64 NVAL 68
 QY 1 NVAL 5

Search completed: Thu Jul 30 11:00:22 1998
 Job time : 7 secs.

Db 87 NPYAL 91
| | | |
QY 1 NPYAL 5

RESULT 2
ID P73988 PRELIMINARY; PRT; 215 AA.
AC P73988;

DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT 01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 23.8 KD PROTEIN.
OS SYNECHOCYSTIS SP.
OC EUBACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCYSTIS.







RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PCC6803;
RA TABATA S.;
RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PCC6803;
RA KANERO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
RA MIYAJIMA N., HIROGAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
RA HOSOUCHI T., MATSUO A., MURAKI A., NAKAZAKI N., NARDO K.,
RA OKUMURA S., SHIMO S., TAKEUCHI C., WADA T., WATANABE A.,
RA YAMADA M., YASUDA M., TABATA S.;
RL DNA RES. 3:109-136(1996).
DR EMBL; D90911; G1653142; -.
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 215 AA; 23768 MW; 329FA3F6 CRC32;

Query Match 100.0%; Score 35; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.56e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 128 NPYAL 132
| | | |
QY 1 NPYAL 5

Search completed: Thu Jul 30 11:01:07 1998
Job time : 26 secs.

Query Match 100.0%; Score 95; DB 9; Length 36;
 Best Local Similarity 100.0%; Pred. No. 6.12e-03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 LKKLQDVHNFVA 36
 |||||
 QY 1 LKKLQDVHNFVA 13

RESULT

ID R58052 standard; peptide; 36 AA.

AC R58052:

DE 20-SEP-1994 (first entry)

DE [L8,A17,Q18,A19]-hPTH(1-36)-OH.

KW Human parathyroid hormone; hPTH; variant; analogue;

KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;

OS hypoparathyroidism.

OS Synthetic.

GB2269176-A.

02-FEB-1994.

12-JUL-1993.

PR 15-JUL-1992; GB-01384.

PR 18-DEC-1992; GB-013009.

PR 23-DEC-1992; GB-026415.

PR 23-DEC-1992; GB-026859.

PR 28-JAN-1993; GB-026861.

PR 28-JAN-1993; GB-001691.

PR 14-APR-1993; GB-001692.

PR 19-APR-1993; GB-007673.

PR 19-APR-1993; GB-008033.

PA (SANO) SANDOZ LTD.

PA (BAUER) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.

PI (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;

PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

PI Maelchli R, Rainer A;

DR WPI; 94-018352/03.

PT New active para-thyroid hormone variants - used for treating or

PT preventing osteoporosis etc.

PS Example 45; Page 36; 92pp; English.

CC This peptide is an example of a highly generic formula covering

CC parathyroid hormone variants useful for treating or preventing bone

CC conditions associated with calcium depletion/resorption, in cases

CC where calcium fixation is required (esp. osteoporosis) or to treat

CC hypoparathyroidism.

SQ Sequence 36 AA;

Query Match 100.0%; Score 95; DB 9; Length 36;
 Best Local Similarity 100.0%; Pred. No. 6.12e-03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 LKKLQDVHNFVA 36
 |||||
 QY 1 LKKLQDVHNFVA 13

Search completed: Thu Jul 30 11:04:57 1998
 Job time : 22 secs.

WISREH (TM)

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MPsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:03:49 1998; MasPar time 3.36 Seconds
Tabular output not generated. 141.457 Million cell updates/sec

Title: >US-08-817-547A-28
Description: (1-13) from US08817547A.pep
Perfect Score: 95
Sequence: 1 LRKKLDVHNFEVA 13

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr56
1:plr1 2:plr2 3:plr3 4:plr4 5:nrl3d

Statistics: Mean 26.057; Variance 41.730; scale 0.624

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	
2	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	
3	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	
4	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	
5	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	
6	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	
7	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	
8	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	
9	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	
10	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	
11	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	
12	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	
13	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	
14	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	
15	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	
16	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	
17	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	
18	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	
19	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	
20	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	
21	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	
22	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	
23	95	100.0	34	5	12WE parathyroid hormone (1.21e-06	

24	56	58.9	445	2	S43492	surface antigen - hep	1.83e+01
25 <td>55</td> <td>57.9<td>102</td><td>2</td><td>S53076</td><td>probable membrane pro</td><td>2.63e+01</td></td>	55	57.9 <td>102</td> <td>2</td> <td>S53076</td> <td>probable membrane pro</td> <td>2.63e+01</td>	102	2	S53076	probable membrane pro	2.63e+01
26 <td>55</td> <td>57.9<td>119</td><td>2</td><td>A34937</td><td>parathyroid hormone p</td><td>2.63e+01</td></td>	55	57.9 <td>119</td> <td>2</td> <td>A34937</td> <td>parathyroid hormone p</td> <td>2.63e+01</td>	119	2	A34937	parathyroid hormone p	2.63e+01
27 <td>55</td> <td>57.9</td> <td>203</td> <td>2</td> <td>S20584</td> <td>DNA-directed RNA poly</td> <td>2.63e+01</td>	55	57.9	203	2	S20584	DNA-directed RNA poly	2.63e+01
28 <td>55</td> <td>57.9</td> <td>227</td> <td>2</td> <td>A24911</td> <td>prolactin-like protein</td> <td>2.63e+01</td>	55	57.9	227	2	A24911	prolactin-like protein	2.63e+01
29 <td>55</td> <td>57.9</td> <td>305</td> <td>2</td> <td>C64864</td> <td>hypothetical protein</td> <td>2.63e+01</td>	55	57.9	305	2	C64864	hypothetical protein	2.63e+01
30 <td>55</td> <td>57.9</td> <td>453</td> <td>2</td> <td>S59436</td> <td>hypothetical protein</td> <td>2.63e+01</td>	55	57.9	453	2	S59436	hypothetical protein	2.63e+01
31 <td>55</td> <td>57.9</td> <td>462</td> <td>2</td> <td>A42401</td> <td>microphage elastase (</td> <td>2.63e+01</td>	55	57.9	462	2	A42401	microphage elastase (2.63e+01
32 <td>55</td> <td>57.9</td> <td>911</td> <td>2</td> <td>S28098</td> <td>stef protein - f1s310</td> <td>2.63e+01</td>	55	57.9	911	2	S28098	stef protein - f1s310	2.63e+01
33 <td>54</td> <td>56.8</td> <td>154</td> <td>2</td> <td>S03242</td> <td>hypothetical protein</td> <td>3.75e+01</td>	54	56.8	154	2	S03242	hypothetical protein	3.75e+01
34 <td>54</td> <td>56.8</td> <td>179</td> <td>2</td> <td>I40594</td> <td>DNA-directed DNA poly</td> <td>3.75e+01</td>	54	56.8	179	2	I40594	DNA-directed DNA poly	3.75e+01
35 <td>54</td> <td>56.8</td> <td>189</td> <td>2</td> <td>S59264</td> <td>hypothetical protein</td> <td>3.75e+01</td>	54	56.8	189	2	S59264	hypothetical protein	3.75e+01
36 <td>54</td> <td>56.8</td> <td>342</td> <td>2</td> <td>S51402</td> <td>probable membrane pro</td> <td>3.75e+01</td>	54	56.8	342	2	S51402	probable membrane pro	3.75e+01
37 <td>54</td> <td>56.8</td> <td>421</td> <td>2</td> <td>ISRYA</td> <td>Seryl-trna synthetase</td> <td>3.75e+01</td>	54	56.8	421	2	ISRYA	Seryl-trna synthetase	3.75e+01
38 <td>54</td> <td>56.8</td> <td>421</td> <td>2</td> <td>ISRYB</td> <td>Seryl-trna synthetase</td> <td>3.75e+01</td>	54	56.8	421	2	ISRYB	Seryl-trna synthetase	3.75e+01
39 <td>54</td> <td>56.8</td> <td>421</td> <td>2</td> <td>S38948</td> <td>Seryl-trna synthetase</td> <td>3.75e+01</td>	54	56.8	421	2	S38948	Seryl-trna synthetase	3.75e+01
40 <td>54</td> <td>56.8</td> <td>421</td> <td>2</td> <td>ISRYA</td> <td>Seryl-trna synthetase</td> <td>3.75e+01</td>	54	56.8	421	2	ISRYA	Seryl-trna synthetase	3.75e+01
41 <td>54</td> <td>56.8</td> <td>421</td> <td>2</td> <td>ISRYB</td> <td>Seryl-trna synthetase</td> <td>3.75e+01</td>	54	56.8	421	2	ISRYB	Seryl-trna synthetase	3.75e+01
42 <td>54</td> <td>56.8</td> <td>421</td> <td>2</td> <td>ISRYB</td> <td>Seryl-trna synthetase</td> <td>3.75e+01</td>	54	56.8	421	2	ISRYB	Seryl-trna synthetase	3.75e+01
43 <td>54</td> <td>56.8</td> <td>421</td> <td>2</td> <td>ISRYB</td> <td>Seryl-trna synthetase</td> <td>3.75e+01</td>	54	56.8	421	2	ISRYB	Seryl-trna synthetase	3.75e+01
44 <td>54</td> <td>56.8</td> <td>421</td> <td>2</td> <td>ISRYB</td> <td>Seryl-trna synthetase</td> <td>3.75e+01</td>	54	56.8	421	2	ISRYB	Seryl-trna synthetase	3.75e+01
45 <td>54</td> <td>56.8</td> <td>752</td> <td>2</td> <td>S51866</td> <td>Hpr1 protein - yeast</td> <td>3.75e+01</td>	54	56.8	752	2	S51866	Hpr1 protein - yeast	3.75e+01

ALIGNMENTS

RESULT	1	12WE	#type complete
ENTRY		parathyroid hormone (residues 4-37) - human	
TITLE		HPTH(4-37)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 4-37, NMR 10	
PDB_TITLE		structures	
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67860	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WE	
REFERENCE		TN001721	
#book		Marx, U.C.	
COMMENT		In Strukturen Verschiedener Parathormonfragmente in Loesung,	
COMMENT		pp.0, Bayreuth: University of Bayreuth (thesis), 1996	
KEYWORDS		Resolution: not applicable	
FEATURES		Determination: NMR	
15-25		hormone	
SUMMARY		#region helix (right hand alpha)	
		length 34 #molecular-weight 4128 #checksum 5508	
Query Match		100.0%; Score 95; DB 5; Length 34;	
Best Local Similarity		100.0%; Pred. No. 1.21e-06;	
Matches		13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	21	LRKKLDVHNFEVA 33	
Qy	1	LRKKLDVHNFEVA 13	
RESULT	2	12WE	#type complete
ENTRY		parathyroid hormone 4-37 mutant N-TERMINAL SUCCINYLATED -	
TITLE		synthetic	
ALTERNATE_NAMES		n-succinyl-hPTH(4-37)	
PDB_TITLE		succinyl human parathyroid hormone 4-37, NMR, 10 structures	
ORGANISM		#formal_name synthetic	
REFERENCE		A67743	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WE	
REFERENCE		TN003319	
#book		Marx, U.C.	
COMMENT		In Strukturen Verschiedener Parathormonfragmente in Loesung,	
COMMENT		pp.0, Bayreuth: University of Bayreuth (thesis), 1996	
		Resolution: not applicable	

Thu Jul 30 13:38:09 1998

US-08-817-547A-28.rpr

Page 2

```
COMMENT      Determination: NMR
KEYWORDS      disease mutation; hormone; signal
FEATURE
2-9
15-25
SUMMARY      #region helix (right hand alpha)\
              #region helix (right hand alpha)
              #length 34 #molecular-weight 4128 #checksum 5508
Query Match      100.0%; Score 95; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.21e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db      21 LKKLQDVHNFVA 33
OY      1 LKKLQDVHNFVA 13
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Search completed: Thu Jul 30 11:04:18 1998
Job time : 29 secs.

Search completed: Thu Jul 30 11:02:48 1998
 Job time : 7 secs.

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OC EUTHERIA; ARTIODACTYLIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 80056617.
RA KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
RL POTTS J.T. JR., RICH A.;
PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 82037785.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83105964.
RA WEAVER C.A., GORDON D.F., KEMPER B.;
MOL. CELL. ENDOCRINOL. 28:411-424(1982).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84262483.
RA WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
GENE 28:319-329(1984).
RN [5]
RP SEQUENCE OF 26-115.
RX MEDLINE; 74142666.
RA HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,
RL COHN D.V.;
PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
RN [6]
RP SEQUENCE OF 32-115.
RX MEDLINE; 71076162.
RA NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DANSON B.F.,
RL AUBACH G.D., POTTS J.T. JR.;
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970).
RN [7]
RP SEQUENCE OF 32-115.
RX MEDLINE; 71063634.
RA BREMER H.B. JR., ROMAN R.;
PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE; 71091588.
RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
RL DEFTOS L.J., DANSON B.F., HOGAN M.L., AUBACH G.D.;
PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL; V00106; G85; -.
DR EMBL; J00023; G163641; -.
DR EMBL; J00024; G163643; -.
DR EMBL; J00024; E18249; ALT_SEQ.
DR EMBL; J00024; E18250; ALT_INIT.
DR EMBL; K0138; G163647; -.
DR EMBL; M25082; G163645; -.
DR PIR; A01534; PTBO.
DR PIR; A24949; A24949.
DR PROSITE; PS00335; PARATHYROID; 1.
KW HORMONE; SIGNAL.
FT SIGNAL 1 25
FT PROPEP 26 31 PARATHYROID HORMONE.
FT CHAIN 32 115 V -> G (IN REF. 4).
FT CONFLICT 106 106
SQ SEQUENCE 115 AA; 12980 MW; 673EA5F2 CRC32;

Query Match 100.0%; Score 95; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 6.50e-09;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 55 LRKLIQDVHNFVA 67
OY 1 LRKLIQDVHNFVA 13

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(a) (b) (c) (d) (e)

RN [2]
 RP COMPLETE GENOME.
 RA YANEZ R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,
 RA RODRIGUEZ J.F., VINUELA E.;
 RL VIROLOGY 208:249-278(1995).
 CC -1- FUNCTION: POLYPROTEIN PP220 IS THE PRECURSOR OF THE MAJOR VIRION
 CC PROTEINS P150, P37, P34 AND P14 OF AFRICAN SWINE FEVER VIRUS.
 DR EMBL: Z22777; G394709; -.
 DR EMBL: U18466; G780461; -.
 KW POLYPROTEIN.
 SQ SEQUENCE 2475 AA; 281479 MW; 6F4E3C0A CRC32;

Query Match 69.5%; Score 66; DB 11; Length 2475;
 Best Local Similarity 75.0%; Pred. No. 4.93e-02;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1944 LKRLQDVISFV 1955

QY 1 LKRLQDVHNFV 12

Search completed: Thu Jul 30 11:03:33 1998
 Job time : 27 secs.

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 LKKLQGVHNFV 35
QY 1 LKKLQGVHNFV 12

RESULT 2

ID R58213 standard; peptide: 36 AA.
AC R58213;
DT 20-SEP-1994 (first entry)
DE [D-Ser17]-hPTH(1-36)-NH₂.
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.
FH Key
FT misc_difference 17 Location/Qualifiers
FT modified_site 36 /note= "D-form residue."
FT /note= "in amide form"

GB2269176-A.
02-FEB-1994.
12-JUL-1993; 014384.
PR 15-JUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026859.
PR 23-DEC-1992; GB-026859.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001691.
PR 14-APR-1993; GB-007673.
PR 19-APR-1993; GB-008033.
PA (SANO) SANDOZ LTD.
PA (BAUE/) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-EPFINDUNGEN VERM GES MBH.
PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Maechli R, Ralner A;
DR WPI; 94-018352/03.

PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
PS Example 211; Page 44; 92pp; English.
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
Sequence 36 AA:

Query Match 100.0%; Score 91; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.17e-02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 LKKLQGVHNFV 35
QY 1 LKKLQGVHNFV 12

Search completed: Thu Jul 30 11:07:36 1998
Job time : 24 secs.

WIDEORH
(TM)

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Msrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:06:37 1998; MasPar time 3.31 Seconds
Tabular output not generated. 132.368 Million cell updates/sec

Title: >US-08-817-547A-29
Description: (1-12) from US08817547A.dep
Perfect Score: 91
Sequence: 1 LRRKLDVHNFV 12

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

pir56
1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 25.786; Variance 40.708; scale 0.633

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Suit No.	Score	Query Match	Length	ID	Description	Pred. No.
1	91	100.0	34	5 12WE	parathyroid hormone (4.58e-06	
2	91	100.0	34	5 12WC	parathyroid hormone (4.58e-06	
3	91	100.0	34	5 12WF	parathyroid hormone (4.58e-06	
4	91	100.0	34	5 12WD	parathyroid hormone (4.58e-06	
5	91	100.0	36	5 12WB	parathyroid hormone (4.58e-06	
6	91	100.0	37	5 12WH	parathyroid hormone (4.58e-06	
7	91	100.0	37	5 12WC	parathyroid hormone (4.58e-06	
8	91	100.0	115	2 A05091	parathyroid hormone p 4.58e-06	
9	91	100.0	115	1 PTHU	parathyroid hormone p 4.58e-06	
10	91	100.0	115	1 PTHC	parathyroid hormone p 4.58e-06	
11	91	100.0	115	1 PTHB	parathyroid hormone p 4.58e-06	
12	91	100.0	115	1 PTHA	parathyroid hormone p 4.58e-06	
13	84	92.3	34	5 12WA	parathyroid hormone (1.16e-04	
14	84	92.3	34	5 12WB	parathyroid hormone (1.16e-04	
15	81	89.0	105	2 I51851	cyclic parathyroid ho 4.52e-04	
16	66	72.5	2475	2 S35307	polypeptide hormone - 2.87e-01	
17	60	65.9	444	2 S09881	citrate transport pro 3.14e+00	
18	58	63.7	183	2 S42547	glucose-1-phosphate a 6.77e+00	
19	58	63.7	330	2 I51545	myc protein - African 6.77e+00	
20	57	62.6	419	1 TVXLMC	transforming protein 6.77e+00	
21	58	62.6	281	2 S41854	phosphoprotein phosph 9.88e+00	
22	57	62.6	525	2 C64313	hypothetical protein 9.88e+00	
23	55	60.4	119	2 A34937	parathyroid hormone p 2.08e+01	

24	55	60.4	305	2	C64864	hypothetical protein	2.08e+01
25 <td>55</td> <td>60.4<td>445<td>2</td><td>S43492</td><td>surface antigen - hep</td><td>2.08e+01</td></td></td>	55	60.4 <td>445<td>2</td><td>S43492</td><td>surface antigen - hep</td><td>2.08e+01</td></td>	445 <td>2</td> <td>S43492</td> <td>surface antigen - hep</td> <td>2.08e+01</td>	2	S43492	surface antigen - hep	2.08e+01
26 <td>55</td> <td>60.4<td>453<td>2</td><td>S59436</td><td>hypothetical protein</td><td>2.08e+01</td></td></td>	55	60.4 <td>453<td>2</td><td>S59436</td><td>hypothetical protein</td><td>2.08e+01</td></td>	453 <td>2</td> <td>S59436</td> <td>hypothetical protein</td> <td>2.08e+01</td>	2	S59436	hypothetical protein	2.08e+01
27 <td>55</td> <td>60.4<td>462<td>2</td><td>A42401</td><td>macrophage elastase (</td><td>2.08e+01</td></td></td>	55	60.4 <td>462<td>2</td><td>A42401</td><td>macrophage elastase (</td><td>2.08e+01</td></td>	462 <td>2</td> <td>A42401</td> <td>macrophage elastase (</td> <td>2.08e+01</td>	2	A42401	macrophage elastase (2.08e+01
28 <td>55</td> <td>60.4<td>911<td>2</td><td>S28098</td><td>st66 protein - fission</td><td>2.08e+01</td></td></td>	55	60.4 <td>911<td>2</td><td>S28098</td><td>st66 protein - fission</td><td>2.08e+01</td></td>	911 <td>2</td> <td>S28098</td> <td>st66 protein - fission</td> <td>2.08e+01</td>	2	S28098	st66 protein - fission	2.08e+01
29 <td>54</td> <td>59.3<td>102</td><td>2</td><td>S53076</td><td>probable membrane pro</td><td>2.99e+01</td></td>	54	59.3 <td>102</td> <td>2</td> <td>S53076</td> <td>probable membrane pro</td> <td>2.99e+01</td>	102	2	S53076	probable membrane pro	2.99e+01
30 <td>54</td> <td>59.3<td>154</td><td>2</td><td>S03242</td><td>hypothetical protein</td><td>2.99e+01</td></td>	54	59.3 <td>154</td> <td>2</td> <td>S03242</td> <td>hypothetical protein</td> <td>2.99e+01</td>	154	2	S03242	hypothetical protein	2.99e+01
31 <td>54</td> <td>59.3<td>179</td><td>2</td><td>I40594</td><td>DNA-directed DNA poly</td><td>2.99e+01</td></td>	54	59.3 <td>179</td> <td>2</td> <td>I40594</td> <td>DNA-directed DNA poly</td> <td>2.99e+01</td>	179	2	I40594	DNA-directed DNA poly	2.99e+01
32 <td>54</td> <td>59.3<td>189</td><td>2</td><td>S59264</td><td>hypothetical protein</td><td>2.99e+01</td></td>	54	59.3 <td>189</td> <td>2</td> <td>S59264</td> <td>hypothetical protein</td> <td>2.99e+01</td>	189	2	S59264	hypothetical protein	2.99e+01
33 <td>54</td> <td>59.3<td>342</td><td>2</td><td>S51402</td><td>probable membrane pro</td><td>2.99e+01</td></td>	54	59.3 <td>342</td> <td>2</td> <td>S51402</td> <td>probable membrane pro</td> <td>2.99e+01</td>	342	2	S51402	probable membrane pro	2.99e+01
34 <td>54</td> <td>59.3<td>421</td><td>5</td><td>1SERB</td><td>Seryl-<i>t</i>-RNA synthetase</td><td>2.99e+01</td></td>	54	59.3 <td>421</td> <td>5</td> <td>1SERB</td> <td>Seryl-<i>t</i>-RNA synthetase</td> <td>2.99e+01</td>	421	5	1SERB	Seryl- <i>t</i> -RNA synthetase	2.99e+01
35 <td>54</td> <td>59.3<td>421</td><td>5</td><td>1SRXB</td><td>Seryl-<i>t</i>-RNA synthetase</td><td>2.99e+01</td></td>	54	59.3 <td>421</td> <td>5</td> <td>1SRXB</td> <td>Seryl-<i>t</i>-RNA synthetase</td> <td>2.99e+01</td>	421	5	1SRXB	Seryl- <i>t</i> -RNA synthetase	2.99e+01
36 <td>54</td> <td>59.3<td>421</td><td>5</td><td>1SERB</td><td>Seryl-<i>t</i>-RNA synthetase</td><td>2.99e+01</td></td>	54	59.3 <td>421</td> <td>5</td> <td>1SERB</td> <td>Seryl-<i>t</i>-RNA synthetase</td> <td>2.99e+01</td>	421	5	1SERB	Seryl- <i>t</i> -RNA synthetase	2.99e+01
37 <td>54</td> <td>59.3<td>421</td><td>5</td><td>1SERB</td><td>Seryl-<i>t</i>-RNA synthetase</td><td>2.99e+01</td></td>	54	59.3 <td>421</td> <td>5</td> <td>1SERB</td> <td>Seryl-<i>t</i>-RNA synthetase</td> <td>2.99e+01</td>	421	5	1SERB	Seryl- <i>t</i> -RNA synthetase	2.99e+01
38 <td>54</td> <td>59.3<td>421</td><td>5</td><td>1SERB</td><td>Seryl-<i>t</i>-RNA synthetase</td><td>2.99e+01</td></td>	54	59.3 <td>421</td> <td>5</td> <td>1SERB</td> <td>Seryl-<i>t</i>-RNA synthetase</td> <td>2.99e+01</td>	421	5	1SERB	Seryl- <i>t</i> -RNA synthetase	2.99e+01
39 <td>54</td> <td>59.3<td>421</td><td>5</td><td>S38948</td><td>Seryl-<i>t</i>-RNA synthetase</td><td>2.99e+01</td></td>	54	59.3 <td>421</td> <td>5</td> <td>S38948</td> <td>Seryl-<i>t</i>-RNA synthetase</td> <td>2.99e+01</td>	421	5	S38948	Seryl- <i>t</i> -RNA synthetase	2.99e+01
40 <td>54</td> <td>59.3<td>421</td><td>5</td><td>1SERB</td><td>Seryl-<i>t</i>-RNA synthetase</td><td>2.99e+01</td></td>	54	59.3 <td>421</td> <td>5</td> <td>1SERB</td> <td>Seryl-<i>t</i>-RNA synthetase</td> <td>2.99e+01</td>	421	5	1SERB	Seryl- <i>t</i> -RNA synthetase	2.99e+01
41 <td>54</td> <td>59.3<td>421</td><td>5</td><td>1SERB</td><td>Seryl-<i>t</i>-RNA synthetase</td><td>2.99e+01</td></td>	54	59.3 <td>421</td> <td>5</td> <td>1SERB</td> <td>Seryl-<i>t</i>-RNA synthetase</td> <td>2.99e+01</td>	421	5	1SERB	Seryl- <i>t</i> -RNA synthetase	2.99e+01
42 <td>54</td> <td>59.3<td>752</td><td>2</td><td>S51866</td><td>HPRI protein - yeast</td><td>2.99e+01</td></td>	54	59.3 <td>752</td> <td>2</td> <td>S51866</td> <td>HPRI protein - yeast</td> <td>2.99e+01</td>	752	2	S51866	HPRI protein - yeast	2.99e+01
43 <td>53<td>58.2</td><td>348</td><td>2</td><td>S45890</td><td>ODPI protein - yeast</td><td>4.29e+01</td></td>	53 <td>58.2</td> <td>348</td> <td>2</td> <td>S45890</td> <td>ODPI protein - yeast</td> <td>4.29e+01</td>	58.2	348	2	S45890	ODPI protein - yeast	4.29e+01
44 <td>53<td>58.2</td><td>500</td><td>2</td><td>C64043</td><td>citrate (pro-3S)-lyase</td><td>4.29e+01</td></td>	53 <td>58.2</td> <td>500</td> <td>2</td> <td>C64043</td> <td>citrate (pro-3S)-lyase</td> <td>4.29e+01</td>	58.2	500	2	C64043	citrate (pro-3S)-lyase	4.29e+01
45 <td>53<td>58.2</td><td>569</td><td>2</td><td>S62851</td><td>MG397 homolog D02_orf</td><td>4.29e+01</td></td>	53 <td>58.2</td> <td>569</td> <td>2</td> <td>S62851</td> <td>MG397 homolog D02_orf</td> <td>4.29e+01</td>	58.2	569	2	S62851	MG397 homolog D02_orf	4.29e+01

ALIGNMENTS

RESULT	ENTRY	12WE	#type complete
TITLE	parathyroid hormone (residues 4-37) - human		
ALTERNATE_NAMES	HPTH(4-37)		
PDB_TITLE	structure of human parathyroid hormone fragment 4-37, NMR 10 structures		
ORGANISM	#formal_name Homo sapiens #common_name man		
REFERENCE	A67860 Roesch, P.; Marx, U.C.		
#authors	submitted to the Brookhaven Protein Data Bank, June 1996		
#cross-references	PDB:12WE		
REFERENCE	TN001721 Marx, U.C.		
#book	In Strukturen Verschiedener Parathormonfragmente in Loessung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996		
COMMENT	Resolution: not applicable		
KEYWORDS	hormone		
FEATURE			
SUMMARY	#region helix (right hand alpha) #length 34 #molecular-weight 4128 #checksum 5508		
Query Match	100.0%; Score 91; DB 5; Length 34;		
Best Local Similarity	100.0%; Pred. No. 4.58e-06;		
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
DB	21 LRRKLDVHNFV 32		
QY	1 LRRKLDVHNFV 12		
RESULT	2		
ENTRY	12WC	#type complete	
TITLE	parathyroid hormone 4-37 mutant N-TERMINAL SUCCINYLATED -		
ALTERNATE_NAMES	n-succinyl-npth(4-37)		
PDB_TITLE	succinyl human parathyroid hormone 4-37, NMR, 10 structures		
ORGANISM	#formal_name synthetic		
REFERENCE	A67743 Roesch, P.; Marx, U.C.		
#authors	submitted to the Brookhaven Protein Data Bank, June 1996		
#cross-references	PDB:12WC		
REFERENCE	TN003319 Marx, U.C.		
#book	In Strukturen Verschiedener Parathormonfragmente in Loessung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996		
COMMENT	Resolution: not applicable		

Thu Jul 30 13:38:10 1998

US-08-817-547A-29.rpr

```
COMMENT      Determination: NMR
KEYWORDS      disease mutation: hormone; signal
FEATURE
2-9
15-25
SUMMARY      #region helix (right hand alpha)\
              #region helix (right hand alpha)
              #length 34 #molecular-weight 4128 #checksum 5508
Query Match      100.0%; Score 91; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 4,58e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 21 LRRK1QDVHNFV 32
OY 1 LRRK1QDVHNFV 12
```

Search completed: Thu Jul 30 11:06:55 1998
Job time : 18 secs.

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MSPrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:06:12 1998; MasPar time 2.30 Seconds
Tabular output not generated. 130.665 Million cell updates/sec

Title: >US-08-817-547A-29
Description: (1-12) from US08817547A.pep
Perfect Score: 91
Sequence: 1 LRRKKIQDVHNFV 12

Scoring table:
PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 27.047; Variance 34.136; scale 0.792

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	91	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	4.71e-08
2	91	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	4.71e-08
3	91	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	4.71e-08
4	91	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	4.71e-08
5	91	100.0	115	1	PTHY_RAT PARATHYROID HORMONE PR	4.71e-08
6	60	65.9	444	1	CITL_KIEPN CITRATE-PROTON SYMPORT	5.45e-01
7	58	63.7	184	1	GLC2_ANATH GLUCOSE-1-PHOSPHATE AD	1.36e+00
8	58	63.7	419	1	MYC1_XENLA MYC 1 PROTO-ONCOGENE P	1.36e+00
9	57	62.6	281	1	P2C1_YEAST PROTEIN PHOSPHATASE 2C	2.14e+00
10	57	62.6	525	1	Y107_METUA HYPOTHETICAL PROTEIN M	2.14e+00
11	55	60.4	119	1	PTHY_CHICK PARATHYROID HORMONE PR	5.16e+00
12	55	60.4	162	1	Y4XD_RHISN HYPOTHETICAL 18.0 KD P	5.16e+00
13	55	60.4	305	1	HLVE_ECOLI HEMOLYSIN E (HEMOLYSIN	5.16e+00
14	55	60.4	462	1	COGM_MOUSE MACROPHAGE METALLOELAS	5.16e+00
15	55	60.4	911	1	STB6_SCHPO STE6 PROTEIN.	5.16e+00
16	55	60.4	1053	1	UBA3_WHEAT UBIQUITIN-ACTIVATING E	5.16e+00
17	54	59.3	102	1	YM88_YEAST VERY HYPOTHETICAL 11.8	7.94e+00
18	54	59.3	154	1	Y1K7_SSV1 HYPOTHETICAL 17.8 KD P	7.94e+00
19	54	59.3	189	1	YNOO_YEAST VERY HYPOTHETICAL 21.7	7.94e+00
20	54	59.3	233	1	DP3E_BUCAP DNA POLYMERASE III, EP	7.94e+00
21	54	59.3	421	1	SYS_THETH SERYL-TRNA SYNTHETASE	7.94e+00
22	54	59.3	752	1	HPRI_YEAST HPRI PROTEIN.	7.94e+00
23	54	59.3	926	1	KINH_NEUCR KINESIN HEAVY CHAIN.	7.94e+00

RESULT	ID	PTHY_BOVIN	STANDARD;	PRT;	115 AA.	ALIGNMENTS
AC	P01268:					
DT	21-JUL-1986	(REL. 01, CREATED)				
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).					
GN	PTH.					
OS	BOS TAURUS (BOVINE).					
CC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
OC	EUTHERIA; ARTIODACTYLA.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	WEAVER C.A., GORDON D.F., MCDEVITT B.E., MAJZUB J.A., NATHANS J., SHARP P.A.,					
RL	MOL. CELL. ENDOCRINOL. 28:411-424(1982).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RA	WEAVER C.A., GORDON D.F., KEMPER B.;					
RL	MEDLINE; 82037785.					
RL	PROC. NATL. ACAD. SCI. U.S.A. 76:4073-4077(1981).					
RN	[3]					
RP	SEQUENCE FROM N.A.					
RA	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;					
RL	GENE 28:319-329(1984).					
RN	[4]					
RP	SEQUENCE OF 26-115.					
RA	HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,					
RL	CORN D.V.;					
RN	[6]					
RP	SEQUENCE OF 32-115.					
RA	NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,					
RL	AUBACH C.D., POTTS J.T. JR.,					
RN	[7]					
RP	SEQUENCE OF 32-115.					
RA	HOPPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).					
RL	MEDLINE; 71063634.					

Thu Jul 30 13:38:10 1998

US-08-817-547A-29.rsp

Search completed: Thu Jul 30 11:06:18 1998
Job time : 6 secs.

Page 2

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RA BREMER H.B. JR., RONAN R.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).  
RN [8]  
RP SYNTHESIS OF 32-65.  
RX MEDLINE: 71091588.  
RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NALL H.D., SAUER R.,  
RL DEFOS L.J., DAWSON B.F., HOGAN M.L., AUBRACH G.D.;  
CC PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).  
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
DR BONE AND PREVENTING THEIR RENAL EXCRETION.  
DR EMBL: V00106; G85; -  
DR EMBL: J00023; G163641; -  
DR EMBL: J00024; G163643; -  
DR EMBL: J00024; E18248; -  
DR EMBL: J00024; E18250; ALT-SEQ.  
DR EMBL: K01938; G163647; -  
DR EMBL: M25082; G163647; -  
DR PIR: A01534; PMDO.  
DR PIR: A24949; A24949.  
PROSITE: PS00335; PARATHYROID; 1.  
HORMONE; SIGNAL.  
FT PROPEP 1 25  
FT CHAIN 26 31  
FT CONFLICT 32 115  
SQ SEQUENCE 106 105 PARATHYROID HORMONE.  
Query Match V -> G (IN REF. 4).  
Best Local Similarity 100.08; Score 91; DB 1; Length 115;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 55 LRRKLDVHNFV 66  
OY 1 LRRKLDVHNFV 12  
RESULT 2  
ID PTH CANFA STANDARD; PRT: 115 AA.  
AC P52212;  
DT 01-OCT-1996 (REL. 34, CREATED)  
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).  
GN PTH.  
OS CANIS FAMILIARIS (DOG).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.  
RN [1]  
SEQUENCE FROM N.A.  
TX TISSUE-PARATHYROID;  
RA ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,  
RL DENVILLE J.W., CAPEN C.C.; -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
CC GENE 160:241-243(1995).  
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
DR BONE AND PREVENTING THEIR RENAL EXCRETION.  
DR EMBL: U15662; G558916; -  
DR PROSITE: PS00335; PARATHYROID; 1.  
KM HORMONE; SIGNAL.  
FT SIGNAL 1 25  
FT PROPEP 26 31  
FT CHAIN 32 115 BY SIMILARITY.  
SQ SEQUENCE 115 AA; 12957 MW; 16DDEBC CRC32; PARATHYROID HORMONE.  
Query Match  
Best Local Similarity 100.08; Score 91; DB 1; Length 115;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 55 LRRKLDVHNFV 66  
OY 1 LRRKLDVHNFV 12
```


Thu Jul 30 13:38:11 1998

US-08-817-547A-29.rsp

Page 2

```
RN [2]
RP COMPLETE GENOME.
RA YANEZ R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,
RL RODRIGUEZ J.F., VINUELA E.,
CC VIROLOGY 208:249-278(1995).
CC -I- FUNCTION: POLYPROTEIN PP220 IS THE PRECURSOR OF THE MAJOR VIRION
DR PROTEINS P150, P37, P94 AND P14 OF AFRICAN SWINE FEVER VIRUS.
DR EMBL: 222777; G394709; -.
KW POLYPROTEIN
SQ SEQUENCE 2475 AA: 281479 MW: 6F4E3C0A CRC32;

Query Match
Best Local Similarity 72.5%; Score 66; DB 11; Length 2475;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1944 LRRKLDVISEFV 1955
OY 1 LRRKLDVHNFV 12
```

Search completed: Thu Jul 30 11:05:54 1998
Job time : 39 secs.

M O S E R
(TW)

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Masrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:10:20 1998; Maspar time 2.67 Seconds
63.142 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-30
Description: (1-11) from US08817547A.pep
Perfect Score: 84
Sequence: 1 LRKKLQDVHNF 11

Scoring table: PAM 150
Gap 15

Searched: 124785 segs, 1538987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 18.206; Variance 59.063; scale 0.308

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	84	100.0	34 26	R62432	Accelerator peptide b	4.45e-02
2	84	100.0	34 22	W17957	Human parathyroid hor	4.45e-02
3	84	100.0	34 22	W17956	Human parathyroid hor	4.45e-02
4	84	100.0	34 22	W17958	Human parathyroid hor	4.45e-02
5	84	100.0	34 22	W17959	Human parathyroid hor	4.45e-02
6	84	100.0	34 7	R34363	Human parathyroid hor	4.45e-02
7	84	100.0	36 9	R58182	[Nva8]-hPTH(1-36)-NH2	4.45e-02
8	84	100.0	36 9	R58184	[Tyr18]-hPTH(1-36)-NH2	4.45e-02
9	84	100.0	36 9	R58179	[Leu1]-hPTH(1-36)-NH2	4.45e-02
10	84	100.0	36 9	R58069	Isopropyl-1-[L8,K(Isopr	4.45e-02
11	84	100.0	36 9	R58285	[Ala23]-hPTH(1-36)-NH	4.45e-02
12	84	100.0	36 9	R58074	[L8,Y18]-hPTH(1-36)-O	4.45e-02
13	84	100.0	44 26	P30015	Human parathyroid hor	4.45e-02
14	84	100.0	84 27	W25687	Human parathyroid hor	4.45e-02
15	84	100.0	84 4	R23523	Human parathyroid hor	4.45e-02
16	84	100.0	84 4	R23447	Porcine parathyroid h	4.45e-02
17	84	100.0	84 4	R23253	Bovine parathyroid ho	4.45e-02
18	84	100.0	84 9	R49695	Sequence of variant c	4.45e-02
19	84	100.0	84 4	R23444	Porcine parathyroid h	4.45e-02

20	84	100.0	84 4	R21221	Human parathyroid hor	4.45e-02
21	84	100.0	84 4	R23463	Porcine parathyroid h	4.45e-02
22	84	100.0	84 4	R21201	Human parathyroid hor	4.45e-02
23	84	100.0	84 4	R21200	Human parathyroid hor	4.45e-02
24	84	100.0	84 4	R21203	Human parathyroid hor	4.45e-02
25	84	100.0	84 4	R21202	Human parathyroid hor	4.45e-02
26	84	100.0	84 4	R23376	Bovine parathyroid ho	4.45e-02
27	84	100.0	84 4	R23464	Porcine parathyroid h	4.45e-02
28	84	100.0	84 4	R23366	Bovine parathyroid ho	4.45e-02
29	84	100.0	84 4	R23365	Bovine parathyroid ho	4.45e-02
30	84	100.0	84 4	R23354	Bovine parathyroid ho	4.45e-02
31	84	100.0	84 4	R23545	Bovine parathyroid ho	4.45e-02
32	84	100.0	84 4	R21206	Human parathyroid hor	4.45e-02
33	84	100.0	84 4	R21207	Human parathyroid hor	4.45e-02
34	84	100.0	84 4	R23233	Human parathyroid hor	4.45e-02
35	84	100.0	84 4	R21220	Human parathyroid hor	4.45e-02
36	84	100.0	84 4	R23311	Bovine parathyroid ho	4.45e-02
37	84	100.0	84 4	R23510	Porcine parathyroid h	4.45e-02
38	84	100.0	84 4	R23255	Bovine parathyroid ho	4.45e-02
39	84	100.0	84 5	R29562	Oxidation resistant l	4.45e-02
40	84	100.0	84 5	R28846	Bovine parathyroid ho	4.45e-02
41	84	100.0	84 4	R23380	Bovine parathyroid ho	4.45e-02
42	84	100.0	84 4	R23381	Bovine parathyroid ho	4.45e-02
43	84	100.0	84 4	R23418	Porcine parathyroid h	4.45e-02
44	84	100.0	84 4	R23323	Bovine parathyroid ho	4.45e-02
45	84	100.0	115 4	P40251	Protein sequence incl	4.45e-02

ALIGNMENTS

RESULT 1
ID R62432 standard; peptide; 34 AA.

AC R62432;
DT 31-JUL-1995 (first entry)
DE Accelerator peptide basic region peptide, P-8
KW Accelerator; basic amino acid; cell growth factor; growth; gingiva;
KW Periodontal tissue; regeneration; periodontitis; periodontal pocket;
KW down growth; epithelium; fibre adhesion; cement.
OS Synthetic.

PN J06234653-AA.
PD 23-AUG-1994.
PF 10-FEB-1993; 045998.
PR 10-FEB-1993; JP-045998.
PA (SUNZ) SUNSTAR CHEM IND CO LTD.
DR WPI; 95-157631/21.

PT Accelerator for regenerating periodontal tissue - comprises
PT peptide having 3-34 aminoacid residues having connected basic
PT aminoacid residues
PS Disclosure; Page 3; 7pp; Japanese.

CC The sequences in R62425-36 are peptide fragments of an accelerator
CC protein which contain at least two basic amino acids. The accelerator
CC also comprises a cell growth factor. The accelerator may be used to
CC accelerate the growth of periodontal tissue regeneration. The
CC accelerator is applied by opening the gingiva, treating the tissue
CC destroyed by periodontitis and applying the accelerator in the
CC periodontal pocket. The accelerator reduces the down growth of the
CC epithelium and accelerates fibre adhesion and regenerates cement.
SQ Sequence 34 AA;

Query Match 100.0%; Score 84; DB 26; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.45e-02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 LRKKLQDVHNF 34
|||||
QY 1 LRKKLQDVHNF 11

RESULT 2
ID W17957 standard; peptide; 34 AA.
AC W17957;
DT 29-JUL-1997 (first entry)

DE Human parathyroid hormone analogue [Ala3]hPTH(1-34)NH2.

KW Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
KW bone fracture.
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_site 3 /label= Alb
FT modified_site 34
FT modified_site 34 /note= "in amide form"
FT WO9702834-A1.
PN 30-JAN-1997.
PD 03-JUL-1996; U11282.
PF 13-JUL-1995; US-001105.
PR 06-SEP-1995; US-003305.
PR 29-MAR-1996; US-626186.
PA (BIOM-) BIOMESURE INC.
PI Dong ZX:
PI MPI; 97-118819/11.
PT New variants of human parathyroid hormone 1-34 peptide - which stimulate bone growth and are used for treatment of osteoporosis and bone fracture
Claim 11; Page -: 33pp; English.
CC The present sequence is a specific example of a human parathyroid hormone (hPTH) analogue from fragment 1-34 in which at least one of the amino acid residues at positions 3, 12, 16, 17, 19 and 34 is alpha-aminoisobutyric acid (Alb). In this example the Ser residue at position 3 of the wild-type has been substituted by Alb. The hPTH analogues stimulate bone growth and so are useful in human or veterinary medicine for treatment of osteoporosis and bone fracture, optionally in conjunction with anti-resorptive therapy (bisphosphonates and calcitonin).
CC N.B. The present sequence does not appear in the specification. It
CC corresponds to the known hPTH 1-34 fragment with the modifications
CC as stated in the claim.
SQ Sequence 34 AA;
Query Match 100.0%; Score 84; DB 22; Length 34;
Best Local Similarity 100.0%; Pred. No. 4,45e-02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 24 LKKLGDVHNF 34
| | | | | | | | | |
QY 1 LKKLQDVHNF 11

Search completed: Thu Jul 30 11:10:35 1998
Job time : 15 secs.

WIREIMAGE (TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:09:33 1998; MasPar time 3.26 Seconds
Tabular output not generated. 123.270 Million cell updates/sec

Title: >US-08-817-547A-30
Description: (1-11) from US08817547A.pep
Perfect Score: 84
Sequence: 1 LRRKLDVHNF 11

Scoring table:
PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

pir56
1:pir1 2:pir2 3:pir3 4:pir4 5:pir3d

Statistics: Mean 25.053; Variance 38.928; scale 0.644

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	84	100.0	34	5	12WG	4.83e-05
2	84	100.0	34	5	12WF	4.83e-05
3	84	100.0	34	5	12WR	4.83e-05
4	84	100.0	34	5	12WT	4.83e-05
5	84	100.0	34	5	12WU	4.83e-05
6	84	100.0	34	5	12WV	4.83e-05
7	84	100.0	34	5	12WW	4.83e-05
8	84	100.0	34	5	12WX	4.83e-05
9	84	100.0	34	5	12WY	4.83e-05
10	84	100.0	34	5	12WZ	4.83e-05
11	84	100.0	34	5	12WA	4.83e-05
12	84	100.0	34	5	12WB	4.83e-05
13	84	100.0	34	5	12WC	4.83e-05
14	84	100.0	34	5	12WD	4.83e-05
15	84	100.0	34	5	12WE	4.83e-05
16	84	100.0	34	5	12WF	4.83e-05
17	84	100.0	34	5	12WG	4.83e-05
18	84	100.0	34	5	12WH	4.83e-05
19	84	100.0	34	5	12WI	4.83e-05
20	84	100.0	34	5	12WJ	4.83e-05
21	84	100.0	34	5	12WK	4.83e-05
22	84	100.0	34	5	12WL	4.83e-05
23	84	100.0	34	5	12WM	4.83e-05

24	54	64.3	189	2	S59264	hypothetical protein	1.83e+01
25	54	64.3 <th>342</th> <th>2</th> <th>S51402</th> <th>probable membrane pro</th> <th>1.83e+01</th>	342	2	S51402	probable membrane pro	1.83e+01
26	54	64.3 <th>421</th> <th>2</th> <th>S38948</th> <th>serine-CRNA ligase (</th> <th>1.83e+01</th>	421	2	S38948	serine-CRNA ligase (1.83e+01
27	54	64.3 <th>421</th> <th>5</th> <th>ISRYA</th> <th>Seryl-trna synthetase</th> <th>1.83e+01</th>	421	5	ISRYA	Seryl-trna synthetase	1.83e+01
28	54	64.3 <th>421</th> <th>5</th> <th>ISRYB</th> <th>Seryl-trna synthetase</th> <th>1.83e+01</th>	421	5	ISRYB	Seryl-trna synthetase	1.83e+01
29	54	64.3 <th>421</th> <th>5</th> <th>ISRYC</th> <th>Seryl-trna synthetase</th> <th>1.83e+01</th>	421	5	ISRYC	Seryl-trna synthetase	1.83e+01
30	54	64.3 <th>421</th> <th>5</th> <th>ISRYD</th> <th>Seryl-trna synthetase</th> <th>1.83e+01</th>	421	5	ISRYD	Seryl-trna synthetase	1.83e+01
31	54	64.3 <th>421</th> <th>5</th> <th>ISRYE</th> <th>Seryl-trna synthetase</th> <th>1.83e+01</th>	421	5	ISRYE	Seryl-trna synthetase	1.83e+01
32	54	64.3 <th>421</th> <th>5</th> <th>ISRYF</th> <th>Seryl-trna synthetase</th> <th>1.83e+01</th>	421	5	ISRYF	Seryl-trna synthetase	1.83e+01
33	54	64.3 <th>421</th> <th>5</th> <th>ISRYG</th> <th>Seryl-trna synthetase</th> <th>1.83e+01</th>	421	5	ISRYG	Seryl-trna synthetase	1.83e+01
34	54	64.3 <th>421</th> <th>5</th> <th>ISRYH</th> <th>Seryl-trna synthetase</th> <th>1.83e+01</th>	421	5	ISRYH	Seryl-trna synthetase	1.83e+01
35	53	63.1 <th>102</th> <th>2</th> <th>S53076</th> <th>probable membrane pro</th> <th>2.66e+01</th>	102	2	S53076	probable membrane pro	2.66e+01
36	53	63.1 <th>127</th> <th>2</th> <th>A24911</th> <th>prolactin-like protei</th> <th>2.66e+01</th>	127	2	A24911	prolactin-like protei	2.66e+01
37	53	63.1 <th>348</th> <th>2</th> <th>S45890</th> <th>ODP1 protein - yeast</th> <th>2.66e+01</th>	348	2	S45890	ODP1 protein - yeast	2.66e+01
38	53	63.1 <th>500</th> <th>2</th> <th>C64043</th> <th>citrate (pro-35)-lys</th> <th>2.66e+01</th>	500	2	C64043	citrate (pro-35)-lys	2.66e+01
39	53	63.1 <th>569</th> <th>2</th> <th>S62851</th> <th>MG397 homolog D02-ori</th> <th>3.84e+01</th>	569	2	S62851	MG397 homolog D02-ori	3.84e+01
40	52	61.9 <th>571</th> <th>2</th> <th>S38485</th> <th>urase (EC 3.5.1.5) 6</th> <th>3.84e+01</th>	571	2	S38485	urase (EC 3.5.1.5) 6	3.84e+01
41	52	61.9 <th>878</th> <th>2</th> <th>S20486</th> <th>paramyosin - fruit fl</th> <th>3.84e+01</th>	878	2	S20486	paramyosin - fruit fl	3.84e+01
42	52	61.9 <th>879</th> <th>2</th> <th>S22028</th> <th>paramyosin, standard</th> <th>3.84e+01</th>	879	2	S22028	paramyosin, standard	3.84e+01
43	52	61.9 <th>957</th> <th>2</th> <th>C69463</th> <th>type I restriction-eno</th> <th>5.35e+01</th>	957	2	C69463	type I restriction-eno	5.35e+01
44	51	60.7 <th>360</th> <th>2</th> <th>B45734</th> <th>Hisc - Lactococcus la</th> <th>5.35e+01</th>	360	2	B45734	Hisc - Lactococcus la	5.35e+01
45	51	60.7 <th>431</th> <th>1</th> <th>ZTEC3</th> <th>citrate utilization d</th> <th>5.35e+01</th>	431	1	ZTEC3	citrate utilization d	5.35e+01

ALIGNMENTS

RESULT	1	12WG	#type complete
ENTRY	parathyroid hormone 4	parathyroid hormone 4	mutant N-TERMINAL SUCCINYLATED -
TITLE	synthetic	synthetic	
ALTERNATE_NAMES	n-succinyl-hpnh(4-37)		
PDB_TITLE	succinyl human parathyroid hormone 4-37, NMR, 10 structures		
ORGANISM	formal_name synthetic		
REFERENCE	A67743		
#authors	Roesch, P.; Marx, U.C.		
#submission	submitted to the Brookhaven Protein Data Bank, June 1996		
#cross-references	PDB:12WG		
REFERENCE	TN003319		
#authors	Marx, U.C.		
#book	In Strukturen Verschiedener Parathormonfragmente in Loessung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996		
COMMENT	Resolution: not applicable		
KEYWORDS	determination: NMR		
FEATURE	disease mutation; hormone; signal		
2-9			
15-25			
SUMMARY	#region helix (right hand alpha)\		
	#region helix (right hand alpha)		
	length 34 #molecular-weight 4128 #checksum 5508		
Query Match	100.0%; Score 84; DB 5; Length 34;		
Best Local Similarity	100.0%; Pred. No. 4.83e-05;		
Matches	11; Conservative 0; Mismatches 0; Gaps 0;		
DB	21 LRRKLDVHNF 31		
QY	1 LRRKLDVHNF 11		
RESULT	2		
ENTRY	12WF	#type complete	
TITLE	parathyroid hormone 4	37 mutant N-TERMINAL ACETYLATED -	
ALTERNATE_NAMES	n-acetyl-hpnh(4-37)		
PDB_TITLE	structure of n-terminal acetylated human parathyroid hormone, NMR, 10 structures		
ORGANISM	formal_name synthetic		
REFERENCE	A67742		
#authors	Roesch, P.; Marx, U.C.		
#submission	submitted to the Brookhaven Protein Data Bank, June 1996		
#cross-references	PDB:12WF		
REFERENCE	TN003318		
#authors	Marx, U.C.		
#book	In Strukturen Verschiedener Parathormonfragmente in Loessung,		

W I S E N H (TM)

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Search: protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:07:53 1998; Maspar time 2.18 Seconds
Tabular output not generated. 126,596 Million cell updates/sec

Title: >US-08-817-547A-30
Description: (1-11) from US08817547A.pep
Perfect Score: 84
Sequence: 1 LRRKLDVHNF 11

Scoring table:
PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Lasting first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 26.284; Variance 32.770; scale 0.802

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	84	100.0	115	1	PTHY_BOVIN	9.02e-07
2	84	100.0	115	1	PTHY_CANFA	9.02e-07
3	84	100.0	115	1	PTHY_PIG	9.02e-07
4	84	100.0	115	1	PTHY_RAT	9.02e-07
5	84	100.0	115	1	PTHY_HUMAN	9.02e-07
6	60	71.4	444	1	CITL_KLEPN	2.85e-01
7	57	67.9	184	1	GIGC_ARATH	1.17e+00
8	55	65.5	119	1	PTHY_CHICK	2.91e+00
9	55	65.5	162	1	Y4XD_RHNS	2.91e+00
10	55	65.5	305	1	HLYE_ECOLI	2.91e+00
11	55	65.5	462	1	COGK_MOUSE	2.91e+00
12	54	64.3	189	1	YNOO_YEAST	4.36e+00
13	54	64.3	233	1	DP3E_BUCAP	4.56e+00
14	54	64.3	421	1	SYS_THETH	4.56e+00
15	54	64.3	752	1	HPRI_YEAST	4.56e+00
16	53	63.1	102	1	YMB8_YEAST	7.08e+00
17	53	63.1	227	1	PRRA_RAT	7.08e+00
18	53	63.1	348	1	HMTI_YEAST	7.08e+00
19	53	63.1	500	1	CILA_HAEIN	7.08e+00
20	53	63.1	569	1	Y397_MYCPN	1.09e+01
21	52	61.9	571	1	UREI_STAXY	1.09e+01
22	52	61.9	621	1	Y04E_MYCTU	1.09e+01
23	52	61.9	879	1	MYSP_DROME	1.09e+01

RESULT	ID	PTHY_BOVIN	STANDARD:	PRT:	115 AA.	ALIGNMENTS
AC	P01268:					
DT	21-JUL-1986 (REL. 01, CREATED)					
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)					
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)					
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).					
GN	PTH.					
OS	BOS TAURUS (BOVINE).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
OC	EUTHERIA; ARTIODACTYLA.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE: 80056617.					
RA	KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,					
RA	POTTS J.T., JR., RICH A.J.					
RL	PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE: 82037785.					
RA	WEAVER C.A., GORDON D.F., KEMPER B.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).					
RN	[3]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE: 83105964.					
RA	WEAVER C.A., GORDON D.F., KEMPER B.;					
RL	MOL. CELL. ENDOCRINOL. 28:411-424(1982).					
RN	[4]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE: 84262483.					
RA	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;					
RL	GENE 28:319-329(1984).					
RN	[5]					
RP	SEQUENCE OF 26-115.					
RX	MEDLINE: 74142665.					
RA	HAMILTON J.W., NITALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T., JR.,					
RL	COHN D.V.;					
RN	PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).					
RP	SEQUENCE OF 32-115.					
RX	MEDLINE: 71076162.					
RA	NITALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,					
RA	AURACH G.D., POTTS J.T., JR.;					
RL	HOPPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).					
RN	[7]					
RP	SEQUENCE OF 32-115.					
RX	MEDLINE: 71063634.					

Search completed: Thu Jul 30 11:08:00 1998
Job time : 7 secs.

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RA BREWER H.B. JR., RONAN R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE: 71091588.
RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,
RA DEFLOS L.J., DAMSON B.F., HOGAN M.L., AUBACH G.D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL: J00106; 683; -
DR EMBL: J00023; G163641; -
DR EMBL: J00024; G163643; -
DR EMBL: J00024; E18249; ALT_SEQ.
DR EMBL: J00024; E18250; ALT_INIT.
DR EMBL: K01938; G163647; -
DR EMBL: M25082; G163645; -
DR PIR: A01534; PTRO.
DR PIR: A24949; A24949.
DR PROSITE: PS00335; PARATHYROID; 1.
DR HORMONE; SIGNAL.
SQ SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115
FT CONFLICT 106 106 V -> G (IN REF. 4).
SQ SEQUENCE 115 AA; 12980 MW; 673EA5F2 CRC32;

Query Match
Best Local Similarity 100.0%; Score 84; DB 1; Length 115;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 55 LRRKLDVHNF 65
QY 1 LRRKLDVHNF 11

RESULT 2
ID ID PTHY-CANFA STANDARD; PRT; 115 AA.
AC P5212;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.
OS CANTIS PAMILIARIS (DOG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; CARNIVORA.
RN [1]
RN SEQUENCE FROM N.A.
RN TISSUE-PARATHYROID;
RN MEDLINE: 95369696.
RA ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,
RA DENTLE J.W., CAPEN C.C.;
RL GENE 160:241-243(1995).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL: U15662; G558916; -
DR PROSITE: PS00335; PARATHYROID; 1.
DR HORMONE; SIGNAL.
KW HORMONE; SIGNAL.
FT SIGNAL 1 25
FT PROPEP 26 31 BY SIMILARITY.
FT CHAIN 32 115 BY SIMILARITY.
SQ SEQUENCE 115 AA; 12957 MW; 16ED0EBC CRC32;

Query Match
Best Local Similarity 100.0%; Score 84; DB 1; Length 115;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 55 LRRKLDVHNF 65
QY 1 LRRKLDVHNF 11

```

M O S E R
(TW)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:08:17 1998; Maspar time 3.90 Seconds
118.655 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-30
Description: (1-11) from US08817547A.pep
Perfect Score: 84
Sequence: 1 LRRKLDVHNF 11

Scoring table: PAM 150
Gap 15

Searched: 140542 segs, 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 25.128; Variance 32.322; scale 0.777

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	74	88.1	105	10	PARATHYROID HORMONE (F	2.88e-04
2	59	70.2	2475	11	POLYPEPTIDE PR220.	5.64e-01
3	58	69.0	591	3	F52E10.5 (FRAGMENT).	9.04e-01
4	57	67.9	299	3	SIMILAR TO SER/THR PRO	1.44e+00
5	57	67.9	320	3	HYPOTHETICAL PROTEIN I	1.44e+00
6	56	66.7	1291	2	MRNA (K1AA0067) FOR OR	2.28e+00
7	55	65.5	453	1	HYPOTHETICAL 50.0 KD P	3.60e+00
8	55	65.5	1459	3	R09E10.5.	3.60e+00
9	55	65.5	2708	3	CHLOROQUINE RESISTANCE	3.60e+00
10	55	65.5	2742	3	CHLOROQUINE RESISTANCE	3.60e+00
11	55	65.5	2819	3	STRAIN HB3 CG2 (CG2).	5.65e+00
12	54	64.3	207	11	ORF36L.	5.65e+00
13	54	64.3	342	1	CHROMOSOME XII COSMID	5.65e+00
14	54	64.3	400	3	TEKTIN B1	5.65e+00
15	54	64.3	735	3	C06G3.9 PROTEIN.	5.65e+00
16	53	63.1	265	8	AGL15 TYPE 2.	8.80e+00
17	53	63.1	373	3	C04G6.2 PROTEIN.	8.80e+00
18	53	63.1	398	8	SIMILAR TO SACHCHAROMYC	8.80e+00
19	53	63.1	1744	3	T14G8.1 (FRAGMENT).	8.80e+00
20	52	61.9	90	3	COSMID F11G11.	1.36e+01

21	52	61.9	160	9	ORF 3.	1.36e+01
22	52	61.9	485	3	C13A2.5 PROTEIN.	1.36e+01
23	52	61.9	602	9	OLIGOPEPTIDASE.	1.36e+01
24	52	61.9	929	9	PUTATIVE N6-ADEININE S	1.36e+01
25	52	61.9	957	9	TYPE I RESTRICTION-MOD	1.36e+01
26	52	61.9	1312	2	RADS0	1.36e+01
27	51	60.7	110	4	CAMP-REGULATED PHOSPHO	2.10e+01
28	51	60.7	231	9	ORF10.	2.10e+01
29	51	60.7	242	8	PUTATIVE MADS-BOX FAMI	2.10e+01
30	51	60.7	242	8	MADS-BOX FAMILY TRANSC	2.10e+01
31	51	60.7	257	8	BOX PROTEIN.	2.10e+01
32	51	60.7	317	4	MCI-R PROTEIN	2.10e+01
33	51	60.7	317	4	MELNOCYTE STIMULATING	2.10e+01
34	51	60.7	330	12	MYC PROTEIN (FRAGMENT)	2.10e+01
35	51	60.7	360	9	HISC.	2.10e+01
36	51	60.7	385	3	C38C3.3 PROTEIN.	2.10e+01
37	51	60.7	733	3	TARTAN PROTEIN PRECURS	2.10e+01
38	51	60.7	1200	9	CHROMOSOME SEGREGATION	2.10e+01
39	51	60.7	1444	11	RNA-DEPENDENT RNA POLY	2.10e+01
40	51	60.7	1630	12	MYOMESIN.	2.10e+01
41	51	60.7	2743	2	POLYPOSIS LOCUS-ENCODE	2.10e+01
42	51	60.7	2829	12	ADENOMATOUS POLYPOSIS	2.10e+01
43	51	60.7	2842	10	APC PROTEIN.	2.10e+01
44	51	60.7	2844	2	POLYPOSIS LOCUS-ENCODE	2.10e+01
45	51	60.7	2845	10	ADENOMATOUS POLYPOSIS	2.10e+01

ALIGNMENTS

RESULT	ID	063473	PRELIMINARY:	PRT:	105 AA.
AC	063473;				
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)				
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)				
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE (FRAGMENT).				
GN	PTH.				
OS	RATUUS NORVEGICUS (RAT).				
OC	EUFAROTA; METAFOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
CC	EUROPERIA; RODENTIA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-THYROID, AND PARATHYROID;				
RA	SCHWELZER H.-J., GROSS G., MAYER H.;				
RL	ADV. GENE TECHNOL. 21:228-229(1984).				
DR	EMBL; M54875; G601933; -				
FT	NON TER 1				
SO	SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;				
Query Match		88.1%	Score 74;	DB 10;	Length 105;
Best Local Similarity		90.9%	Pred. No. 2.88e-04;		
Matches	10;	Conservative	0;	Mismatches	1;
Indels	0;	Gaps	0;		
DB	45	LRRKLDVHNF 55			
Qy	1	LRRKLDVHNF 11			
RESULT	2	PRELIMINARY:	PRT:	2475 AA.	
AC	008358				
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)				
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)				
DT	01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)				
DE	POLYPEPTIDE PR220.				
GN	CP2475L.				
OS	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V) (ASFV).				
CC	VIROIDE; DS-DNA NONENVELOPED VIRUSES; IRIDOVIRIDAE.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 93327788.				
RA	SIMON-MATEO C.; ANDRES G.; VINUELA E.;				
RL	EMBO J. 12:2977-2987(1993).				

RN [2]
RP COMPLETE GENOME.
RA YANEZ R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,
RA RODRIGUEZ J.F., VINUELA E.,
RL VIROLOGY 208:249-278(1995).
CC -1- FUNCTION: POLYPROTEIN PP220 IS THE PRECURSOR OF THE MAJOR VIRION
CC PROTEINS P150, P37, P34 AND P14 OF AFRICAN SWINE FEVER VIRUS.
DR EMBL; Z22777; G394709; -.
DR EMBL; U18466; G780461; -.
KM POLYPROTEIN.
SQ SEQUENCE 2475 AA; 281479 MW; 6F4E3C0A CRC32;

Query Match 70.2%; Score 59; DB 11; Length 2475;
Best Local Similarity 72.7%; Pred. No. 5.64e-01;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1944 LRKTLQDVISF 1954
||| ||| :|
QY 1 LRKTLQDVHNF 11

Search completed: Thu Jul 30 11:09:14 1998
Job time : 57 secs.

NWSEEF (TW)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:12:42 1998; MasPar time 2.67 Seconds
57.535 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-31
Description: (1-10) from US08817547A.pep
Perfect Score: 73
Sequence: 1 LRRK1QDVHN 10

Scoring table:
PAM 150
Gap 15

Searched: 124785 segs, 15338987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 17.167; Variance 59.785; scale 0.287

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	73	100.0	33 18	R88841	Human parathyroid hor	8.53e-01
2	73	100.0	34 26	R62432	Accelerator peptide b	8.53e-01
3	73	100.0	34 9	R45508	Parathyroid hormone/p	8.53e-01
4	73	100.0	34 9	R45528	Parathyroid hormone/p	8.53e-01
5	73	100.0	34 13	R69037	PTH analogue with amp	8.53e-01
6	73	100.0	34 7	R34353	Human parathyroid hor	8.53e-01
7	73	100.0	34 7	R34352	Bovine parathyroid ho	8.53e-01
8	73	100.0	34 7	R34345	Bovine parathyroid ho	8.53e-01
9	73	100.0	34 8	R41582	[Arg15,16,17]hPTH (1-	8.53e-01
10	73	100.0	34 22	W20002	Cyclised rat parathyr	8.53e-01
11	73	100.0	34 22	W20003	Cyclised [Nle 8,18, T	8.53e-01
12	73	100.0	34 22	W17962	Human PTH analogue [C	8.53e-01
13	73	100.0	35 14	R74442	Parathyroid hormone p	8.53e-01
14	73	100.0	35 14	R74413	Parathyroid hormone p	8.53e-01
15	73	100.0	35 14	R74527	Human parathyroid hor	8.53e-01
16	73	100.0	36 9	R58243	Propargy1-[Al]-hPTH(1	8.53e-01
17	73	100.0	36 9	R58057	[L8, D10, A16, Q18]-hPTH	8.53e-01
18	73	100.0	36 9	R58026	N-alpha-methyl[Ala1]	8.53e-01
19	73	100.0	36 9	R58177	Morpholine-2-carboxy	8.53e-01

20	73	100.0	38 9	R58089	[Arg12]-hPTH(1-38)-OH	8.53e-01
21	73	100.0	38 9	R58061	[Ile13]-hPTH(1-38)-OH	8.53e-01
22	73	100.0	38 9	R58028	[Cys13]-hPTH(1-38)-OH	8.53e-01
23	73	100.0	38 9	R58028	[Thr11]-hPTH(1-38)-OH	8.53e-01
24	73	100.0	38 9	R58124	[Lys19]-hPTH(1-38)-OH	8.53e-01
25	73	100.0	44 26	P30015	Human parathyroid hor	8.53e-01
26	73	100.0	84 27	W25687	Human parathyroid hor	8.53e-01
27	73	100.0	84 4	R21244	Human parathyroid hor	8.53e-01
28	73	100.0	84 4	R23453	Bovine parathyroid ho	8.53e-01
29	73	100.0	84 4	R23453	Porcine parathyroid h	8.53e-01
30	73	100.0	84 4	R23242	Human parathyroid hor	8.53e-01
31	73	100.0	84 4	R23241	Human parathyroid hor	8.53e-01
32	73	100.0	84 4	R23346	Bovine parathyroid ho	8.53e-01
33	73	100.0	84 4	R23336	Bovine parathyroid hor	8.53e-01
34	73	100.0	84 4	R23529	Human parathyroid hor	8.53e-01
35	73	100.0	84 4	R21217	Human parathyroid hor	8.53e-01
36	73	100.0	84 4	R21198	Human parathyroid hor	8.53e-01
37	73	100.0	84 4	R23251	Bovine parathyroid hor	8.53e-01
38	73	100.0	84 4	R21256	Human parathyroid hor	8.53e-01
39	73	100.0	84 4	R23368	Bovine parathyroid ho	8.53e-01
40	73	100.0	84 6	R30857	Leu18 hPTH mutein.	8.53e-01
41	73	100.0	84 6	R30856	Cys35 hPTH mutein.	8.53e-01
42	73	100.0	84 4	R21241	Human parathyroid hor	8.53e-01
43	73	100.0	84 4	R21240	Human parathyroid hor	8.53e-01
44	73	100.0	84 4	R23474	Human parathyroid hor	8.53e-01
45	73	100.0	84 4	R23475	Porcine parathyroid h	8.53e-01

ALIGNMENTS

RESULT 1
ID R88841 standard; peptide; 33 AA.

AC R88841;
DT 07-OCT-1996 (first entry)
DE Human parathyroid hormone analogue, [Leu27]-hPTH(1-33)-NH2.
KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;
KW calcium regulation; reduced PKC activity; protein kinase C;
KW increased adenylyl cyclase activity; cAMPase; bone loss.
OS Synthetic.
FH Key
FT modified_site 33 Location/Qualifiers
FT CA2126299-A.
FN 21-DEC-1995.
PD 20-JUN-1994; 126299.
PR 20-JUN-1994; CA-126299.
PA (WILL/) WILLICK G E.
PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;
PI Willick GE;
DR WPL: 96-151754/16.
PT New human parathyroid hormone analogues - which have increased
PT adenylyl cyclase activating activity, used for treating osteoporosis
PS Claim 2; Page -: 21pp; English.
CC R88829-R88841 are human parathyroid hormone (PTH) analogues. The
CC analogues increase G-protein coupled adenylyl cyclase (cAMPase) C
CC activity and reduce protein kinase C (PKC) activity. The analogues
CC can reverse the loss of bone and increase bone mass and density
CC without undesirable effects. They are useful for the treatment of
CC osteoporosis and other bone related disorders and disorders
CC involving bone cell calcium regulation.
SQ Sequence 33 AA.

Query Match 100.0%; Score 73; DB 18; Length 33;
Best Local Similarity 100.0%; Pred. No. 8.53e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;







DB 24 lrrk1qdvhn 33
QY 1 LRRK1QDVHN 10

RESULT 2
ID R62432 standard; peptide; 34 AA.

AC R62432: (first entry)
DT 31-JUL-1995
DE Accelerator peptide basic region peptide, p-8.
KW Accelerator; basic amino acid; cell growth factor; growth; gingiva;
KW periodontal tissue; regeneration; periodontitis; periodontal pocket;
KW down growth; epithelium; fibre adhesion; cement.
OS Synthetic.
PN J06234653-A.
PD 23-AUG-1994.
PF 10-FEB-1993; 045998.
PR 10-FEB-1993; JP-045998.
PA (SUWZ) SUNSTAR CHEM IND CO LTD.
DR WPI; 95-157631/21.
PT Accelerator for regenerating periodontal tissue - comprises
PT peptide having 3-34 aminoacid residues having connected basic
PT aminoacid residues
PS Disclosure; Page 3; 7pp; Japanese.
CC The sequences in R62425-36 are peptide fragments of an accelerator
CC protein which contain at least two basic amino acids. The accelerator
CC also comprises a cell growth factor. The accelerator may be used to
CC accelerate the growth of periodontal tissue regeneration. The
CC accelerator is applied by opening the gingiva, treating the tissue
CC destroyed by periodontitis and applying the accelerator in the
CC periodontal pocket. The accelerator reduces the down growth of the
CC epithelium and accelerates fibre adhesion and regenerates cement.
SQ Sequence 34 AA;

Query Match 100.0%; Score 73; DB 26; Length 34;
Best Local Similarity 100.0%; Pred.No. 8.33e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 24 LKKKIQDVHN 33
|||
QY 1 LRRKLDVHN 10

Search completed: Thu Jul 30 11:13:00 1998
Job time : 18 secs.

COMMENT pp. 0, Bayreuth : University of Bayreuth (Thesis), 1996
 COMMENT Resolution: not applicable
 KEYWORDS Determination: NMR
 FEATURE disease mutation; hormone; signal
 3-6
 14-27
 SUMMARY #region helix (right hand alpha) \
 #region helix (right hand alpha) \
 #length 34 #molecular-weight 4128 #checksum 5508
 Query Match 100.0%; Score 73; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.82e-03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 21 LRRKLQDVHN 30
 |||||
 0y 1 LRRKLQDVHN 10

Search completed: Thu Jul 30 11:12:24 1998
 Elapsed time : 17 secs.

Thu Jul 30 13:38:13 1998

 Maspar, using Smith-Waterman algorithm
 of Edinburgh, U.K.
 Ford Molecular Ltd

 116.179 Million cell updates/sec
 Maspar time 2.16 Seconds

 release08817547A.pep
 Cof N 10

 Maspar
 2. segs, 25083644 residues
 Minimum Match 0%
 Listing first 45 summaries
 1:swiss1
 Database:
 swiss-prot35

Statistics: Mean 25.075; Variance 30.505; scale 0.822

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Built No.	Score	Query Match	Length	ID	Description	Pred. No.
1	73	100.0	115	1	PTHY_BOVIN	8.74e-05
2	73	100.0	115	1	PTHY_CANFA	8.74e-05
3	73	100.0	115	1	PTHY_PIG	8.74e-05
4	73	100.0	115	1	PTHY_RAT	8.74e-05
5	73	100.0	115	1	PTHY_HUMAN	8.74e-05
6	73	100.0	115	1	PTHY_CHICK	8.74e-05
7	73	100.0	115	1	PTHY_MOUSE	8.74e-05
8	73	100.0	115	1	PTHY_FISH	8.74e-05
9	73	100.0	115	1	PTHY_BIRD	8.74e-05
10	73	100.0	115	1	PTHY_REPT	8.74e-05
11	73	100.0	115	1	PTHY_AMPH	8.74e-05
12	73	100.0	115	1	PTHY_MOLL	8.74e-05
13	73	100.0	115	1	PTHY_NEMAT	8.74e-05
14	73	100.0	115	1	PTHY_PLANT	8.74e-05
15	73	100.0	115	1	PTHY_FUNG	8.74e-05
16	73	100.0	115	1	PTHY_VIRUS	8.74e-05
17	73	100.0	115	1	PTHY_BACTER	8.74e-05
18	73	100.0	115	1	PTHY_EUKARY	8.74e-05
19	73	100.0	115	1	PTHY_MITOCH	8.74e-05
20	73	100.0	115	1	PTHY_PLASTID	8.74e-05
21	73	100.0	115	1	PTHY_CHLORO	8.74e-05
22	73	100.0	115	1	PTHY_VACUOL	8.74e-05
23	73	100.0	115	1	PTHY_CENTRIO	8.74e-05

RESULT	1	STANDARD	PRT	115 AA.
24	48	65.8	419	1
25	48	65.8	669	1
26	48	65.8	857	1
27	48	65.8	920	1
28	48	65.8	1126	1
29	48	65.8	1263	1
30	48	65.8	100	1
31	47	64.4	112	1
32	47	64.4	189	1
33	47	64.4	752	1
34	47	64.4	911	1
35	47	64.4	1036	1
36	47	64.4	1225	1
37	47	64.4	297	1
38	46	63.0	326	1
39	46	63.0	457	1
40	46	63.0	475	1
41	46	63.0	590	1
42	46	63.0	637	1
43	46	63.0	637	1
44	46	63.0	637	1
45	46	63.0	1679	1

ALIGNMENTS

ID	PTHY_BOVIN	STANDARD	PRT	115 AA.
AC	P01268;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).			
GN	PTH.			
OS	BOS TAURUS (BOVINE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; ARTIODACTYLA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 80056617.			
RA	KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,			
RA	POTTS J.T. JR., RICH A.;			
RL	PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 82037785.			
RA	WEAVER C.A., GORDON D.F., KEMPER B.;			
RA	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;			
RL	MOL. CELL. ENDOCRINOL. 28:411-424(1982).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 84262483.			
RA	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;			
RA	GENE 28:319-329(1984).			
RN	[5]			
RP	SEQUENCE OF 26-115.			
RX	MEDLINE; 74142666.			
RA	HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,			
RA	COHN D.V.;			
RL	PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).			
RN	[6]			
RP	SEQUENCE OF 32-115.			
RX	MEDLINE; 71076162.			
RA	NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,			
RA	AUBACH G.D., POTTS J.T. JR.;			
RL	HOPPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).			
RN	[7]			
RP	SEQUENCE OF 32-115.			
RX	MEDLINE; 71063634.			

Thu Jul 30 13:38:13 1998

US-08-817-547A-31.RSP

Search completed: Thu Jul 30 11:11:00 1998
Job time : 7 secs.

RA BREWER H B JR, RONAN R.;
RN PROC NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RX MEDICINE; 71091588.
RA POTTS J.T. JR.
RU DEFOS L.J. JR.
CC -I- FINEART: PTH. SCI. U.S. HOGAN M. A. 68:63-67(1971).
DR BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL; J00024; G163641; -
DR EMBL; J00024; G163641; -
DR EMBL; K01938; E18250; ALT. SEO.
DR PIR; M25082; G163647; ALT. INIT.
DR PIR; M01534; G163645; -
DR PROSITE; P50033; PTHO.
DR HORMONE; SIGNAL; PARATHYROID; 1.
FT CHAIN 26 25
FT CHAIN 32 31
FT CONFLICT 106 115
SO SEQUENCE 115 AA; 12980 MW; 673EASF2 CRC32;
Query Match Best Local Similarity 100.0%;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 55 LKRLKLDVHN 64
QY 1 LKRLKLDVHN 10
*SULT 2
PTHY CANFA STANDARD; PRT; 115 AA.
OCT-1996 (REL. 34, CREATED)
OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
THYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
PT ETIAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
FT PIVOORA.
SO CHAIN
SEQUENCE
Query Match Best Local Similarity 100.0%;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 55 LKRLKLDVHN 64
QY 1 LKRLKLDVHN 10
*RITY
RITY.
HORMONE.
32;
Length 115;
Indels 0, Gaps 0.

(11)

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 svseiqimhn 10
 |||||
 QY 1 SVSEIQIMHN 10

RESULT 2

ID W17955 standard: peptide; 34 AA.

AC W17955;

DT 29-JUL-1997 (first entry)

DE Human parathyroid hormone analogue [Alb34]hPTH(1-34)NH₂.

KM Osteoporosis; agonist; PTH; human; anti-resorptive therapy;

KM bone fracture.

OS Homo sapiens.

OS Synthetic.

PH key

FT modified_site

PD WO9702834-A1.

PF 30-JAN-1997

PR 03-JUL-1996; U11292

PR 13-JUL-1995; US-001105.

PR 06-SEP-1995; US-003305.

PR 29-MAR-1996; US-626186.

PA (BIOM-) BIOMESURE INC.

PI Dong ZX;

DR WPI; 97-118819/11.

PT New variants of human parathyroid hormone 1-34 peptide - which

PT stimulate bone growth and are used for treatment of osteoporosis and

PT bone fracture

PS Claim 11: Page -: 33pp; English.

CC The present sequence is a specific example of a human parathyroid

CC hormone (hPTH) analogue from fragment 1-34 in which at least one

CC of the amino acid residues at positions 3, 12, 16, 17, 19 and 34

CC is alpha-aminoisobutyric acid (Aib). In this example the phe residue

CC at position 34 of the wild-type has been substituted by Aib. The hPTH

CC analogues stimulate bone growth and so are useful in human or veterinary

CC medicine for treatment of osteoporosis and bone fracture, optionally in

CC conjunction with anti-resorptive therapy (bisphosphonates and

CC calcitonin).

CC N.B. The present sequence does not appear in the specification. It

CC corresponds to the known hPTH 1-34 fragment with the modifications

CC as stated in the claim.

SO Sequence 34 AA;

Query Match 100.0%; Score 68; DB 22; Length 34;

Best Local Similarity 100.0%; Pred.No. 6.37e+00;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 svseiqimhn 10
 |||||
 QY 1 SVSEIQIMHN 10

Search completed: Thu Jul 30 09:58:02 1998
 Job time : 11 secs.







Thu Jul 30 13:37:52 1998

US-08-817-547A-1.RPI

```

17-28      #region helix (right hand alpha) #checksum 3791
SUMMARY      #length 37 #molecular-weight 4401
Query Match 100.0%; Score 68; DB 5; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.43e-04; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;
Db 1 SVSEIOLMHN 10
   |||||
QY 1 SVSEIOLMHN 10

Search completed: Thu Jul 30 09:57:31 1998
Job time : 24 secs.

```

MUSE

(TM)

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Msrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 09:55:44 1998; Maspar time 2.16 Seconds
ular output not generated. 116.271 Million cell updates/sec

Title: >US-08-817-547A-1
Description: (1-10) from US08817547A.pep
Perfect Score: 68
Sequence: 1 SVSEIQLMHN 10

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swissl

Statistics: Mean 23.348; Variance 23.508; scale 0.993

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	68	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	9.25e-06
2	68	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	9.25e-06
3	66	97.1	115	1	PTHY_RAT PARATHYROID HORMONE PR	3.53e-05
4	63	92.6	119	1	PTHY_CHICK PARATHYROID HORMONE PR	2.53e-04
5	61	89.7	115	1	PTHY_CANFA PARATHYROID HORMONE PR	9.17e-04
6	59	86.8	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	3.25e-03
7	50	73.5	369	1	PROB_CORGL GLUTAMATE 5-KINASE (EC	6.99e-01
8	47	69.1	176	1	ARCE_ECOLI ACETYLORNITHINE DEACET	3.65e+00
9	47	69.1	176	1	RETI_ONCMV PLASMA RETINOL-BINDING	3.65e+00
10	47	69.1	176	1	Y413_ARATH HYPOTHETICAL 48.8 KD P	3.65e+00
11	47	69.1	176	1	BR2_YEAST PRE-MRNA SPLICING HELI	6.23e+00
12	46	67.6	175	1	PTHY_MOUSE PARATHYROID HORMONE-RE	1.05e+01
13	45	66.2	175	1	PTHY_CHICK PARATHYROID HORMONE-RE	1.05e+01
14	45	66.2	177	1	PTHY_RAT PARATHYROID HORMONE-RE	1.05e+01
15	45	66.2	177	1	PTHY_CANFA PARATHYROID HORMONE-RE	1.05e+01
16	45	66.2	177	1	PTHY_HUMAN PARATHYROID HORMONE-RE	1.05e+01
17	45	66.2	177	1	PTHY_MOUSE PARATHYROID HORMONE-RE	1.05e+01
18	45	66.2	324	1	IG_GAMMA-1 CHAIN C REG	1.05e+01
19	45	66.2	393	1	IG_GAMMA-1 CHAIN C REG	1.05e+01
20	45	66.2	494	1	PRE-MRNA SPLICING FACT	1.05e+01
21	44	64.7	151	1	LATE EMERGOGENESIS ABU	1.76e+01
22	44	64.7	267	1	DHPS_SNAHA DIHYDROPTEROATE SYNTHA	1.76e+01
23	44	64.7	338	1	THIOSULFATE-BINDING PR	1.76e+01

RESULT	ID	PTHY_HUMAN	STANDARD;	PRT;	115 AA.	ALIGNMENTS
AC	P01270;	21-JUL-1986 (REL. 01, CREATED)				
DT	13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)					
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)					
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).					
GN	PTH.					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
CC	EUTHERIA; PRIMATES.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE; 82150870.					
RA	HENDY G.N., KRONENBERG H.M., POTTS J.T. JR., RICH A.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE; 83169834.					
RA	VASICER T.J., MCCREYTT B.E., FREEMAN M.W., FENNICK B.J.,					
RL	HENDY G.N., POTTS J.T. JR., RICH A., KRONENBERG H.M.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 80:2127-2131(1983).					
RN	[3]					
RP	SEQUENCE OF 26-37.					
RX	MEDLINE; 74174967.					
RA	JACOBS J.W., KEMPER B., NITAL H.D., HABENER J.F., POTTS J.T. JR.;					
RL	NATURE 249:155-157(1974).					
RN	[4]					
RP	SEQUENCE OF 32-68.					
RX	MEDLINE; 74111656.					
RA	NITAL H.D., SAUER R.T., JACOBS J.W., KEUTMANN H.T., SEGRE G.V.,					
RL	O'RIORDAN J.L.H., AURBACH G.D., POTTS J.T. JR.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).					
RN	[5]					
RP	SEQUENCE OF 61-83 AND 84-115.					
RX	MEDLINE; 79082855.					
RA	KEUTMANN H.T., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.,					
RL	POTTS J.T. JR.;					
RL	BIOCHEMISTRY 17:5723-5729(1978).					
RN	[6]					
RP	SEQUENCE OF 75-100.					
RA	KEUTMANN H.T., NITAL H.D., JACOBS J.W., BARLING P.M., HENDY G.N.,					
RL	O'RIORDAN J.L.H., POTTS J.T. JR.;					
RL	(IN) CALCULUM-REGULATING HORMONES, TALMADGE R.V., OWEN M.,					
RL	PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM,					
RL	(1975).					
RN	[7]					

REVOLUTIONS 75146516.
RP MEDLINE: 75146516.
RX KEUTMANN H.T., NIAL H.D., O'RIONDAN J.L.H., POTTS J.T. JR.;
RA BIOCHEMISTRY 14:1842-1847(1975).
RL [8]
RN SYNTHESIS OF 32-65.
RP MEDLINE: 75059420.
RX TREBEAR G.W., VAN RIETSCOTEN J., GREEN E., NIAL H.D., JR.;
RA KEUTMANN H.T., PARSONS J.A., O'RIONDAN J.L.H., POTTS J.T. JR.;
RL HOPE-SEYLER S.Z. PHYSIOL. CHEM. 355:415-421(1974).
RN [9]
RN SYNTHESIS OF 32-65.
RP MEDLINE: 73227467.
RX ANDREATA R.H., HARTMANN A., JOEHL A., KAMBER B., MAIER R.;
RA RINKER B., RITTEL W., STEIER P.;
RL RINKER B., RITTEL W., STEIER P.;
RN HELV. CHIM. ACTA 56:470-473(1973).
RP STRUCTURE BY NMR OF 32-65.
RX MEDLINE: 91299748.
RA KLAUS R., DIECKMANN T., GRAY V., SCHOMBURG D., WINGENDER E., MAYER H.;
RL BIOCHEMISTRY 30:6936-6942(1991).
RN [11]
RP STRUCTURE BY NMR OF 32-65.
RX MEDLINE: 93345518.
RA BARDEN J.A., CUTHBERTSON R.M.;
RL EUR. J. BIOCHEM. 215:315-321(1993).
RN [12]
RP STRUCTURE BY NMR OF 32-68.
RX MEDLINE: 95318094.
RA MARX U.C., AUSTERMANN S., BAYER P., ADELMANN K., ECHART A.,
RL STICHT H., WALTER S., SCHMID F.-X., JAEHNICK R., FORSMANN W.-G.,
RN ROESCH P.;
RX J. BIOL. CHEM. 270:15194-15202(1995).
RL [13]
RN VARIANT ARG-18.
RP MEDLINE: 91009811.
RX ARNOLD A., HORST S.A., GARDELIA T.J., BABA H., LEVINE M.A.;
RA KROENIGER H.M., 86:1084-1087(1990).
RL J. CLIN. INVEST. PTH. ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
RN -1- FUNCTION: PTH. ELEVATES CALCIUM EXCRETION.
RX BONE AND PREVENTING THEIR RENAL EXCRETION.
RA BONE AND PREVENTING THEIR RENAL EXCRETION.
RL -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
RN HYPOPARATHYROIDISM (FTH).
RP EMBL: J00301; G19704; -
RX EMBL: V00597; G31744; -
RA EMBL: A29146; E186700; -
RL PIR: A01536; PTHU.
RN PIR: A19339; A19338.
RP PIR: 1HPH: 10-JUL-85.
RX PIR: 1HTH: 15-OCT-87.
RA PDB: 1ZMA: 12-MAR-97.
RL PDB: 1ZMB: 12-MAR-97.
RN PDB: 1ZMC: 12-MAR-97.
RP PDB: 1ZMD: 12-MAR-97.
RX PDB: 1ZME: 12-MAR-97.
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RL PDB: 1ZMG: 16-JUN-97.
RN PDB: 1ZMH: 16-JUN-97.
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RA PDB: 1ZOC: 16-JUN-97.
RL PDB: 1ZOD: 16-JUN-97.
RN PDB: 1ZOE: 16-JUN-97.
RP PDB: 1ZOF: 16-JUN-97.
RX PDB: 1ZOG: 16-JUN-97.
RA PDB: 1ZOH: 16-JUN-97.
RL PDB: 1ZOI: 16-JUN-97.
RN PDB: 1ZOK: 16-JUN-97.
RP PDB: 1ZOL: 16-JUN-97.
RX PDB: 1ZOM: 16-JUN-97.
RA PDB: 1ZON: 16-JUN-97.
RL PDB: 1ZOO: 16-JUN-97.
RN PDB: 1ZOP:

```

2          STANDARD:          PR: 115 AA.
PTHY_PIG
P01269:
21-JUL-1986 (REL. 01, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
21-JAN-1988 (REL. 33, LAST ANNOTATION UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
PTH SCROFA (PIG).
SUS SCROFA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUMARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; ARTIODACTYLA.
(1)
SEQUENCE FROM N.A.
MEDLINE: 87316938.
WIDERA G., MAIER H.;
SCHNEIDER H.-J., GROSS G.,
NUCLEIC ACIDS RES. 15:6740-6740(1987).
[2]
SEQUENCE OF 26-115.
MEDLINE: 76018954.
CHU L.-H., HUANG W.-Y., LITLEDIKE E.-T., HAMILTON J.-W., COHN D.-V.;
BIOCHEMISTRY 14:3631-3635(1975).
[3]
SEQUENCE OF 32-115.
MEDLINE: 74233317.
O'RIORDAN J.L.H.,
SAIER R.T., NIALL H.D., HOGAN M.L., KEUTMANN H.T.,
PORTS J.T., JR., 1994-1999(1974)
BIOCHEMISTRY 19TH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
-1- FUNCTION: PREVENTING THEIR RENAL EXCRETION.
BONE AND PREVENTING THEIR RENAL EXCRETION.
EMBL: X05722; G839; -.
DR PIR: A01535; PTEG806.
DR PIR: B26806; B26806.
DR PROSITE: P500335; PARATHYROID; 1.
HORMONE; SIGNAL.
25
KWM SIGNAL. 1
FT PROPEP 26 115 PARATHYROID HORMONE.
FT FT 32 115 98B57F47 CRC32:
FT CHAIN 115 AA: 12852 MW:
SEQUENCE 100.0%: DA 1: length 115;
Query Match Similarity 100.0%; Score 68;
Best Local Similarity 100.0%; Pred. NO. 9.25e-06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0
DB 32 SVSEIOLMHN 41
|||||1111
QY 1 SVSEIOLMHN 10
Search completed: Thu Jul 30 09:55:52 1998
Job time : 8 secs.

```

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 on: Thu Jul 30 09:56:12 1998; MasPar time 3.80 Seconds
 110.885 Million cell updates/sec
 Molecular output not generated.

Title:	>US-08-817-547A-1
Description:	(1-10) from US08817547A.pep
Perfect Score:	68
Sequence:	1 SVSEIQLMHN 10

Scoring table: PAM 150
Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: **strembl5**

1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 22.590; Variance 21.849; scale 1.034

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	64	94.1	105	10	Q63473	PARATHYROID HORMONE (F	5.68e-05
2	48	70.6	248	9	Q08320	ACETYLGLUTAMATE KINASE	1.66e+00
3	48	70.6	448	9	Q55883	HYPOTHETICAL 49.8 KD P	1.66e+00
4	48	70.6	1015	2	Q14521	GIANT LARVAE HOMOLOGUE	1.66e+00
5	47	69.1	265	3	Q20456	F46c3.3.	2.96e+00
6	46	67.6	445	2	Q05708	UNDDULIN 2 (MATRIX GLYC	5.23e+00
7	46	67.6	843	10	Q05707	UNDDULIN 1 (MATRIX GLYC	5.23e+00
8	46	67.6	1034	10	Q61856	LEFTAIL GIANT LARVAE HO	5.22e+00
9	46	67.6	1371	9	P73337	SENSORY TRANSDUCTION H	5.15e+00
10	45	66.2	276	3	Q21896	SMILAIR TO TYROSINE KI	9.15e+00
11	45	66.2	405	9	P77215	FROM BASES 2347342 TO	9.15e+00
12	45	66.2	821	9	Q31210	GLYCOCEN PHOSPHORLASE	9.15e+00
13	45	66.2	1405	10	P70366	STEROID RECEPTOR COACT	9.15e+00
14	45	66.2	1405	10	Q61202	STEROID RECEPTOR COACT	9.15e+00
15	45	66.2	1441	2	Q00150	STEROID RECEPTOR COACT	9.15e+00
16	45	66.2	1447	10	P70365	NICLEAR RECEPTOR CO-AC	9.15e+00
17	44	64.7	99	9	Q58911	HYPOTHETICAL 11.5 KD P	1.59e+00
18	44	64.7	287	8	Q08111	FBP6 PROTEIN.	1.59e+00
19	44	64.7	247	8	Q40900	AGAMOUS PROTEIN.	1.59e+00
20	44	64.7	267	9	Q05701	DITHIOPROPERATE SYNTHA	1.59e+00

ID	1	PRELIMINARY:	PRT:	105 AA.
AC	063473;			
DT	01-NOV-1996 (TREMBL,REL. 01, CREATED)			
DT	01-NOV-1996 (TREMBL,REL. 01, LAST SEQUENCE UPDATE)			
DT	01-JAN-1998 (TREMBL,REL. 05, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE (FRAGMENT).			
GN	PTH.			
OS	EUTRUS NORVEGICUS (RAT).			
OC	EUFAROT; METAEOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUHETERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=THYROID, AND PARATHYROID.			
RA	SCHMELZER H.J., GROSS G., MAIER H.;			
RL	ADV. GENE TECHNOL. 21:228-229(1984).			
DR	EMBL: M54875; G601933; -.			
FT	NON_TER			
SO	SEQUENCE	105 AA;	11746 MW;	6AC3163E CAC32;
Query Match				
	Best Local Similarity	94.1%;	Score 64;	DB 10;
	Matches	8;	Conservative	2;
			Mismatches	0;
			Indels	0;
			Gaps	0;
Db	22 AISEIOLMHN 31			
Qy	1 SVSEIOLMHN 10			
RESULT	2	PRELIMINARY:	PRT:	248 AA.
ID	008320;			
AC	008320;			
DT	01-JUL-1997 (TREMBL,REL. 04, CREATED)			
DT	01-JUL-1997 (TREMBL,REL. 04, LAST SEQUENCE UPDATE)			
DT	01-JAN-1998 (TREMBL,REL. 05, LAST ANNOTATION UPDATE)			
DE	ACTYGLUTAMATE KINASE (EC 2.7.2.8).			
GN	ARGB.			
OS	LACTOBACILLUS PLANTARUM.			
OC	PROKARYOTA; FIRMICUTES; REGULAR ASPOROGENOUS ROD; LACTOBACILLACEAE.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-CCM 1904.			
RA	BRINGEL F., FREY L., BOIVIN S., HUBERT J.C.;			
RL	J. BACTERIOL. 179:0-0(1997).			

Thu Jul 30 13:37:52 1998

US-08-817-547A-1.rspt

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CCM 1904;
RA BRINGEL F.;
RL SUBMITTED (AUG-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- CATALYTIC ACTIVITY: ATP + N-ACETYL-L-GLUTAMATE -
CC ADP + N-ACETYL-L-GLUTAMATE 5-PHOSPHATE.
DR EMBL: X99978; E284231; -
KW TRANSFERASE
SQ SEQUENCE 248 AA; 26580 MM; 3E945D79 CRC32;
Query Match 70.6%; Score 48; DB 9; Length 248;
Best Local Similarity 44.4%; Pred. No. 1.66e+00; Indels 0;
Matches 4; Conservative 5; Mismatches 0; Gaps 0;

Db 125 AVNOYQOLMQ 133
OY 1 SYSEIQLMH 9
Search completed: Thu Jul 30 09:56:47 1998
Job time : 35 secs.

M O S E R E F
(TW)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 09:59:58 1998; MasPar time 2.62 Seconds
Molecular output not generated. 52.740 Million cell updates/sec

Title: >US-08-817-547A-2
Description: (1-9) from US08817547A.pep
Perfect Score: 63
Sequence: 1 SVSEIQLMH 9

Scoring table: PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 15.754; Variance 60.392; scale 0.261
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description	Pred. No.
1	63	100.0	34	22	W17954	Human parathyroid hor	9.63e+00
2	63	100.0	34	22	W17955	Human parathyroid hor	9.63e+00
3	63	100.0	34	23	W08127	Human PTH derivative,	9.63e+00
4	63	100.0	34	23	W08102	Parathyroid hormone g	9.63e+00
5	63	100.0	34	7	R34366	Human parathyroid hor	9.63e+00
6	63	100.0	34	7	R34362	Human parathyroid hor	9.63e+00
7	63	100.0	34	20	W14310	Cyclic parathyroid ho	9.63e+00
8	63	100.0	34	20	W14309	Cyclic parathyroid ho	9.63e+00
9	63	100.0	34	22	W17969	Human parathyroid hor	9.63e+00
10	63	100.0	34	22	W17951	Human parathyroid hor	9.63e+00
11	63	100.0	34	22	W17967	Human PTH analogue [C	9.63e+00
12	63	100.0	34	22	W17968	Human parathyroid hor	9.63e+00
13	63	100.0	34	22	W17947	Human parathyroid hor	9.63e+00
14	63	100.0	34	22	W17944	Human parathyroid hor	9.63e+00
15	63	100.0	34	22	W17952	Human parathyroid hor	9.63e+00
16	63	100.0	34	22	W08114	Human PTH derivative,	9.63e+00
17	63	100.0	34	22	W19994	Cyclised human parath	9.63e+00
18	63	100.0	34	7	R34365	Human parathyroid hor	9.63e+00
19	63	100.0	34	7	R34364	Human parathyroid hor	9.63e+00

RESULT	ID	Score	Query Match	length	DB	ID	Description	Pred. No.
20	63	100.0	34	7	R34354	Human parathyroid hor	9.63e+00	
21	63	100.0	34	7	R34353	Human parathyroid hor	9.63e+00	
22	63	100.0	36	9	R58229	[Ala30]-hPTH(1-36)-NH	9.63e+00	
23	63	100.0	36	9	R58298	[NMeVal35]-hPTH(1-36)	9.63e+00	
24	63	100.0	36	9	R58284	[D-Trp23]-hPTH(1-36)-	9.63e+00	
25	63	100.0	36	9	R58242	[Lys(Iso-propyl)13]-hP	9.63e+00	
26	63	100.0	36	9	R58281	[D-Val21]-hPTH(1-36)-	9.63e+00	
27	63	100.0	36	9	R58234	[Ala32]-hPTH(1-36)-NH	9.63e+00	
28	63	100.0	36	9	R58233	[D-His32]-hPTH(1-36)-	9.63e+00	
29	63	100.0	36	8	R39450	Ser-Val-(hPTH 3-35)-P	9.63e+00	
30	63	100.0	36	9	R58274	[Ala15]-hPTH(1-36)-NH	9.63e+00	
31	63	100.0	37	9	R58244	[Ala0]-hPTH(1-36)-NH2	9.63e+00	
32	63	100.0	37	9	R24776	hPTH(1-37)-amide/ethy	9.63e+00	
33	63	100.0	38	9	R58283	[Trp(Pmc)23]-hPTH(1-3	9.63e+00	
34	63	100.0	38	9	R58094	[Trp13]-hPTH(1-38)-OH	9.63e+00	
35	63	100.0	38	9	R58093	[Asn13]-hPTH(1-38)-OH	9.63e+00	
36	63	100.0	38	9	R58166	[Lys33]-hPTH(1-38)-OH	9.63e+00	
37	63	100.0	38	9	R58282	[Trp(SQ2Pmc)23]-hPTH	9.63e+00	
38	63	100.0	38	9	R58061	[Ile15]-hPTH(1-38)-OH	9.63e+00	
39	63	100.0	44	26	P30015	Human parathyroid hor	9.63e+00	
40	63	100.0	44	25	W21946	Fusion protein compri	9.63e+00	
41	63	100.0	84	27	W25687	Human parathyroid hor	9.63e+00	
42	63	100.0	84	25	W29420	Human parathyroid hor	9.63e+00	
43	63	100.0	84	4	R23790	Parathyroid hormone g	9.63e+00	
44	63	100.0	84	5	R23571	Human PTH encoded by	9.63e+00	
45	63	100.0	229	9	R47971	Sequence of a full-le	9.63e+00	

ALIGNMENTS

RESULT 1
ID W17954 standard; peptide; 34 AA.
AC W17954;
DT 29-JUL-1997 (first entry)
DE Human parathyroid hormone analogue [Alb19]hPTH(1-34)NH2.
KW Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
KW bone fracture.
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_site 19
FT modified_site 19 label= Alb
FT modified_site 34
FT modified_site 34 /note= "In amide form"
FN WO9702834-A1.
PD 30-JAN-1997.
PE 03-JUL-1996; U11292.
PR 13-JUL-1995; US-001105.
PR 06-SEP-1995; US-003305.
PR 29-MAR-1996; US-626186.
PA (BIOM-) BIOMEASURE INC.
PI Dong ZX;
DR WPI: 97-118819/11.
PT New variants of human parathyroid hormone 1-34 peptide - which
stimulate bone growth and are used for treatment of osteoporosis and
bone fracture
PS Claim 11: Page -: 33pp; English.
CC The present sequence is a specific example of a human parathyroid
hormone (hPTH) analogue from fragment 1-34 in which at least one
of the amino acid residues at positions 3, 12, 16, 17, 19 and 34
is alpha-aminoisobutyric acid (Aib). In this example the Glu residue
at position 19 of the wild-type has been substituted by Aib. The hPTH
analogues stimulate bone growth and so are useful in human or veterinary
medicine for treatment of osteoporosis and bone fracture, optionally in
conjunction with anti-resorptive therapy (bisphosphonates and
calcitonin).
CC N.B. The present sequence does not appear in the specification. It
corresponds to the known hPTH 1-34 fragment with the modifications
as stated in the claim.
SQ Sequence 34 AA;
Query Match 100.0%; Score 63; DB 22; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.63e+00;

Thu Jul 30 13:38:01 1998

US-08-817-547A-2.rag

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 svseiqjmh 9
 |||||
 QY 1 SVSEIQJLMH 9

RESULT 2

ID W17955 standard; peptide; 34 AA.

AC W17955:

DT 29-JUL-1997 (first entry)

DE Human parathyroid hormone analogue [Alb34]hPTH(1-34)NH₂;

KW Osteoporosis; agonist; PTH; human; anti-resorptive therapy;

KW bone fracture.

OS Homo sapiens.

OS Synthetic.

FT modified_site Location/Qualifiers

Key 34 /label= Alb

note= "in amide form"

NO9702834-A1.

PD 30-JAN-1997. U11292.

PF 03-JUL-1996; US-001105.

PR 13-JUL-1995; US-003305.

PR 06-SEP-1995; US-626186.

PR 29-MAR-1996; US-626186.

PA (BIOM-) BIOMEASURE INC.

PI Dong 2X;

DR WPI; 97-118819/11.

PT New variants of human parathyroid hormone 1-34 peptide - which

stimulate bone growth and are used for treatment of osteoporosis and

bone fracture.

PS Claim 11: Page -: 33pp: English.

CC The present sequence is a specific example of a human parathyroid

hormone (hPTH) analogue from fragment 1-34 in which at least one

of the amino acid residues at positions 3, 12, 16, 17, 19 and 34

is alpha-aminoisobutyric acid (Aib). In this example the Phe residue

at position 34 of the wild-type has been substituted by Aib. The hPTH

analogue stimulate bone growth and so are useful in human or veterinary

medicine for treatment of osteoporosis and bone fracture, optionally in

conjunction with anti-resorptive therapy (bisphosphonates and

calcitonin).

CC N.B. The present sequence does not appear in the specification. It

corresponds to the known hPTH 1-34 fragment with the modifications

as stated in the claim.

CC Sequence 34 AA;

Query Match 100.0%; Score 63; DB 22; Length 34;

Best Local Similarity 100.0%; Pred. No. 9.63e+00;

Matches 9; Conservative 0; Mismatches 0; Indels 0;

Db 1 svseiqjmh 9
 |||||

QY 1 SVSEIQJLMH 9

Search completed: Thu Jul 30 10:00:14 1998
 Job time : 16 secs.

(PL)

US-08-817-547A-2.rpt

Thu Jul 30 13:38:02 1998

```

17-28      #region helix (right hand alpha)
SUMMARY    #length 37 #molecular-weight 4401 #checksum 3791
Query Match      100.0%; Score 63; DB 5; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.58e-03;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db      1 SYSEIQLMH 9
Oy      1 SYSEIQLMH 9

Search completed: Thu Jul 30 09:59:39 1998
Job time : 19 secs.

```

MUSE (TM)

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Msrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Jul 30 09:58:20 1998; Maspar time 2.06 Seconds
Molecular output not generated. 109.762 Million cell updates/sec

Title: >US-08-817-547A-2
Description: (1-9) from US08817547A.pep
Perfect Score: 63
Sequence: 1 SVSEIQLMH 9

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 22.879; Variance 22.094; scale 1.0316

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	63	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	7.43e-05
2	63	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	7.43e-05
3	61	96.8	115	1	PTHY_RAT PARATHYROID HORMONE PR	2.88e-04
4	58	92.1	119	1	PTHY_CHICK PARATHYROID HORMONE PR	2.11e-03
5	56	88.9	115	1	PTHY_CANFA PARATHYROID HORMONE PR	7.68e-03
6	54	85.7	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	2.73e-02
7	50	79.4	369	1	PROB_CORGL GLUTAMATE 5-KINASE (EC	3.16e-01
8	47	74.6	383	1	ARCE_ECOLI ACETYLCHOLINEIN DEACET	1.81e+00
9	47	74.6	435	1	Y413_ARATH HYPOTHETICAL 48.8 KD P	1.81e+00
10	45	71.4	324	1	GCL_MOUSE IG GAMMA-1 CHAIN C REG	5.55e+00
11	45	71.4	393	1	GC14_MOUSE IG GAMMA-1 CHAIN C REG	5.55e+00
12	44	69.8	151	1	LE14_GOSHI LATE EMBRYOGENESIS ABU	9.57e+00
13	44	69.8	553	1	VTEP_BPT3 TAIL FIBER PROTEIN.	9.57e+00
14	44	69.8	557	1	VTEP_BPT7 TAIL FIBER PROTEIN.	9.57e+00
15	43	68.3	103	1	YF17_HAEIN HYPOTHETICAL PROTEIN H	1.63e+01
16	43	68.3	651	1	YHJK_ECOLI HYPOTHETICAL 73.1 KD P	1.63e+01
17	43	68.3	1069	1	ENRK_MOUSE ENTEROPEPTIDASE (EC 3.	1.63e+01
18	43	68.3	1136	1	TIEL_MOUSE TYROSINE-PROTEIN KINAS	1.63e+01
19	43	68.3	1134	1	TIEL_BOVIN TYROSINE-PROTEIN KINAS	1.63e+01
20	43	68.3	2163	1	BRR2_YEAST PRE-mRNA SPLICING HELP	1.63e+01
21	42	66.7	175	1	PTHY_MOUSE PARATHYROID HORMONE-RE	2.76e+01
22	42	66.7	176	1	RET1_ONCMY PLASMA RETINOL-BINDING	2.76e+01
23	42	66.7	176	1	RET2_ONCMY PLASMA RETINOL-BINDING	2.76e+01

RESULT	ID	PTHY_HUMAN	STANDARD:	PRT:	115 AA.	ALIGNMENTS
AC	P01270:					
DT	21-JUL-1986 (REL. 01, CREATED)					
DT	13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)					
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)					
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).					
GN	PTH.					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
OC	EUHETERIA; PRIMATES.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	HENDY G.N., KRONENBERG H.M., POTTS J.T. JR., RICH A.;					
RA	PROC. NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).					
RL	[2]					
RN	SEQUENCE FROM N.A.					
RP	MEDLINE: 83169834.					
RA	VASICER T.J., MCCREYTT B.E., FREEMAN M.W., FENNICK B.J.;					
RA	HENDY G.N., POTTS J.T. JR., RICH A., KRONENBERG H.M.;					
RA	PROC. NATL. ACAD. SCI. U.S.A. 80:2127-2131(1983).					
RL	[3]					
RN	SEQUENCE OF 26-37.					
RP	MEDLINE: 74174967.					
RA	JACOBS J.W., KEMPER B., NIALL H.D., HABENER J.F., POTTS J.T. JR.;					
RA	NATURE 249:155-157(1974).					
RL	[4]					
RN	SEQUENCE OF 32-68.					
RP	MEDLINE: 74111656.					
RA	NIALL H.D., SAUER R.T., JACOBS J.W., KEUTMANN H.T., SEGRE G.V.;					
RA	O'RIORDAN J.L.H., AURBACH G.D., POTTS J.T. JR.;					
RA	PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).					
RL	[5]					
RN	SEQUENCE OF 61-83 AND 84-115.					
RP	MEDLINE: 79082855.					
RA	KEUTMANN H.T., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.;					
RA	POTTS J.T. JR.;					
RA	BIOCHEMISTRY 17:5723-5729(1978).					
RL	[6]					
RN	SEQUENCE OF 75-100.					
RP	KEUTMANN H.T., NIALL H.D., JACOBS J.W., BARLING P.M., HENDY G.N.;					
RA	O'RIORDAN J.L.H., POTTS J.T. JR.;					
RA	(IN) CALCULUM-REGULATING HORMONES, TALMADGE R.V., OWEN M.;					
RA	PARSONS J.A., EDS., PP. 9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM,					
RL	(1975).					
RL	[7]					

RP REVISIONS.
 RX MEDLINE: 75146516.
 RA KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL BIOCHEMISTRY 14:1842-1847(1975).
 RN [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 75059220.
 RA TREGER G.W., VAN RIENSCHOTEN J., GREEN E., NIALL H.D.,
 RA KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T. JR.;
 RL HOPE-SEYLER S.Z. PHYSIOL. CHEM. 355:415-421(1974).
 RN [9]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE: 73227467.
 RA ANDERLETTA R.H., HARTMANN A., JOEHL A., KAMBER B., WALTER R.,
 RA RINKER B., RITTEL W., SIEBER P.;
 RL HELV. CHIM. ACTA 56:470-473(1973).
 RN [10]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE: 91299748.
 RA KLAUS W., DIECKMANN T., WRAY V., SCHOMBURG D., WINGENDER E., MAYER H.;
 RL BIOCHEMISTRY 30:6936-6942(1991).
 RN [11]
 RP STRUCTURE BY NMR OF 32-65.
 RX MEDLINE: 93345518.
 RA BARREN J.A., CUTHBERTSON R.M.;
 RL EUR. J. BIOCHEM. 215:315-321(1993).
 RN [12]
 RP STRUCTURE BY NMR OF 32-68.
 RX MEDLINE: 95318084.
 RA MARK U.C., AUSSERMAN S., BAYER P., ADERMANN K., EICHART A.,
 RA STICHT H., WALTER S., SCHMID F.-X., JAENICKE R., FORSMANN W.-G.,
 RA ROESCH P.;
 RL J. BIOL. CHEM. 270:15194-15202(1995).
 RN [13]
 RP VARIANT ARG-18.
 RX MEDLINE: 91009811.
 RA ARNOID A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,
 RA KRONENBERG H.M.;
 RL J. CLIN. INVEST. 86:1084-1087(1990).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
 CC HYPOPARATHYROIDISM (FTH).
 CC EMBL: J00301; G190704; -;
 DR EMBL: V00597; G37144; -;
 DR EMBL: A29146; E186700; -;
 DR PIR: A01536; PTH.
 DR PIR: A19339; A19339.
 DR PDB: 1HPH: 10-JUL-95.
 DR PDB: 1HTH: 15-OCT-97.
 DR PDB: 1ZMA: 12-MAR-97.
 DR PDB: 1ZMB: 12-MAR-97.
 DR PDB: 1ZMC: 12-MAR-97.
 DR PDB: 1ZMD: 12-MAR-97.
 DR PDB: 1ZME: 12-MAR-97.
 DR PDB: 1ZMF: 16-JUN-97.
 DR PDB: 1ZMG: 16-JUN-97.
 DR MTM: 146200; -;
 DR MTM: 168450; -;
 DR PROSITE: PS00335; PARATHYROID; 1.
 DR HORMONE; SIGNAL; DISEASE MUTATION; 3D-STRUCTURE.
 KW SIGNAL; 1
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT VARIANT 18 18
 FT CONFLICT 107 107
 FT SEQUENCE 115 AA: 12861 MW: 243887C7 CRC32;
 SQ

Query Match 100.0%; Score 63; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 7.43e-05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 32 SVSEIOLMH 40
 QY 1 SVSEIOLMH 9

RESULT 2
 ID PTH_PIG STANDARD; PRT: 115 AA.
 AC P01269;
 DC 21-JUL-1986 (REL. 01, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
 OS PTH.
 GN SUS SCROFA (Pig).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; ARTIODACTYLA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 87316938.
 RA SCHWEIZER H.-J., GROSS G., WIEDER G., MAYER H.;
 RL NUCLEIC ACIDS RES. 15:6740-6740(1987).
 RN [2]
 RP SEQUENCE OF 26-115.
 RX MEDLINE: 76018954.
 RA CHU L.L.H., HUANG W.-Y., LITLEDIKE E.T., HAMILTON J.W., COHN D.V.;
 RL BIOCHEMISTRY 14:3631-3635(1975).
 RN [3]
 RP SEQUENCE OF 32-115.
 RX MEDLINE: 74253317.
 RA SAUER R.T., NIALL H.D., HOGAN M.L., KEUTMANN H.T., O'RIORDAN J.L.H.,
 RA POTTS J.T. JR.;
 RL BIOCHEMISTRY 13:1994-1999(1974).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC EMBL: X05722; G1839; -;
 DR PIR: A01535; PTH.
 DR PIR: B26806; B26806.
 DR PROSITE: PS00335; PARATHYROID; 1.
 DR HORMONE; SIGNAL.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT SEQUENCE 115 AA: 12852 MW: 98867F47 CRC32;
 SQ

Query Match 100.0%; Score 63; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 7.43e-05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: Thu Jul 30 09:58:27 1998
 Job time : 7 secs.

WISCONSIN
(TM)

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MSrch_Pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 09:58:46 1998; MasPar time 3.70 Seconds
Output not generated. 102,472 Million cell updates/sec

Title: >US-08-817-547A-2
Description: (1-9) from US08817547A.pep
Perfect Score: 63
Sequence: 1 SVSEIQLMH 9

Scoring table: PAM 150
Gap 15

Searched: 140542 segs. 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 22.143; Variance 20.804; scale 1.064

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	59	93.7	105	10	063473	PARATHYROID HORMONE (F	6.56e-04
2	48	76.2	248	9	008320	ACETYLGLUTAMATE KINASE	8.60e-01
3	48	76.2	1015	2	014321	GIANT LARVAE HOMOLOGUE	8.60e-01
4	47	74.6	448	9	005883	HYPOTHETICAL 49.8 KD P	1.57e+00
5	46	73.0	445	2	005708	UNIDULIN 2 (MATRIX GLYC	2.85e+00
6	46	73.0	843	2	005707	UNIDULIN 1 (MATRIX GLYC	2.85e+00
7	46	73.0	1034	10	061856	LETHAL GIANT LARVAE HO	2.85e+00
8	45	71.4	276	3	021996	STIMILAR TO TYROSINE KI	5.12e+00
9	45	71.4	1371	3	P73337	SENSORY TRANSDUCTION H	5.12e+00
10	45	71.4	1405	10	061202	STEROID RECEPTOR COACT	5.12e+00
11	45	71.4	1405	10	P70366	STEROID RECEPTOR COACT	5.12e+00
12	45	71.4	1441	2	000150	STEROID RECEPTOR COACT	5.12e+00
13	45	71.4	1447	10	P70365	NUCLEAR RECEPTOR CO-AC	5.12e+00
14	44	69.8	99	9	058811	HYPOTHETICAL 11.5 KD P	9.10e+00
15	44	69.8	407	3	019956	STIMILARITY TO S. CERVI	9.10e+00
16	44	69.8	448	9	031012	ONF51X5 PROTEIN.	9.10e+00
17	44	69.8	821	9	031210	GLYCOGEN PHOSPHORYLASE	9.10e+00
18	43	68.3	167	9	P96578	YDAE PROTEIN.	1.60e+01
19	43	68.3	199	3	018251	Y57G11C.25	1.60e+01
20	43	68.3	225	9	P73618	DEOXIRIBOSE-PHOSPHATE	1.60e+01

RESULT	ID	Score	Query Match	Length	DB	ID	Description	Pred. No.
21	43	66.3	247	8	008711	FBP6 PROTEIN.	1.60e+01	
22	43	66.3	247	8	040900	AGAROSU PROTEIN.	1.60e+01	
23	43	66.3	402	9	055818	HYPOTHETICAL 45.8 KD P	1.60e+01	
24	43	66.3	910	11	011421	HEXON PROTEIN.	1.60e+01	
25	43	66.3	911	11	083905	TERMINAL PROTEIN.	1.60e+01	
26	43	66.3	1057	2	015334	TUMOR SUPPRESSOR PROT	1.60e+01	
27	43	66.3	3456	11	P89201	POLIPROTEIN.	1.60e+01	
28	42	66.7	256	9	026823	CONSERVED PROTEIN.	2.78e+01	
29	42	66.7	405	9	P77215	FROM BASES 2347342 TO	2.78e+01	
30	42	66.7	418	3	026662	VERY EARLY BLASTULA PR	2.78e+01	
31	42	66.7	446	12	P79926	HEPATOCYTE NUCLEAR FAC	2.78e+01	
32	42	66.7	451	8	041789	CALCIUM-DEPENDENT PROT	2.78e+01	
33	42	66.7	487	8	043676	CALCIUM-DEPENDENT PROT	2.78e+01	
34	42	66.7	490	8	042396	CALCIUM-DEPENDENT PROT	2.78e+01	
35	42	66.7	490	8	024430	CALMODULIN-LIKE DOMAIN	2.78e+01	
36	42	66.7	492	8	004417	CALCIUM DEPENDENT PROT	2.78e+01	
37	42	66.7	501	8	038869	CALMODULIN-DOMAIN PROT	2.78e+01	
38	42	66.7	544	8	038872	CALMODULIN-DOMAIN PROT	2.78e+01	
39	42	66.7	556	8	038871	CALMODULIN-DOMAIN PROT	2.78e+01	
40	42	66.7	564	3	020498	F47A4.3.	2.78e+01	
41	42	66.7	573	8	P93838	CALCIUM-DEPENDENT CALM	2.78e+01	
42	42	66.7	579	9	051504	PENICILLIN-BINDING PRO	2.78e+01	
43	42	66.7	646	8	038870	CALMODULIN-DOMAIN PROT	2.78e+01	
44	42	66.7	737	3	017679	C49P5.2.	2.78e+01	
45	42	66.7	2500	3	Q20937	SIMILAR TO S. CEREVISI	2.78e+01	

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	063473	93.7%	Score 59;	DB 10;	Length 105;			
2	063473	Best Local Similarity 77.8%;	Pred. No. 6.56e-04;					
3	063473	Matches 7;	Conservative 2;	Mismatches 0;	Indels 0;	Gaps 0;		
4	063473	1 SVSEIQLMH 9						
5	063473	PRELIMINARY; PRT; 248 AA.						
6	063473	01-JUL-1997 (TREMBLERL. 04, CREATED)						
7	063473	01-JUL-1997 (TREMBLERL. 04, LAST SEQUENCE UPDATE)						
8	063473	01-JAN-1998 (TREMBLERL. 05, LAST ANNOTATION UPDATE)						
9	063473	ACETYLGLUTAMATE KINASE (EC 2.7.2.8).						
10	063473	ARGB.						
11	063473	LACTOBACILLUS PLANTARUM.						
12	063473	PROKARYOTA; FIRMICUTES; REGULAR ASPOROGENOUS ROD; LACTOBACILLACEAE.						
13	063473	SEQUENCE FROM N.A.						
14	063473	STRAIN-CM 1904.						
15	063473	BRINGEL F., FREY L., BOIVIN S., HUBERT J.C..						
16	063473	J. BACTERIOL. 179:0-0(1997).						

Thu Jul 30 13:38:02 1998

US-08-817-547A-2.rsp

Page 2

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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CCM 1904;
RA BRINGEL F.;
RL SUBMITTED (AUG-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- CATALYTIC ACTIVITY: ATP + N-ACETYL-L-GLUTAMATE =
DR EMBL; X99978; E284231; -.
KM TRANSFERASE.
SQ SEQUENCE 248 AA; 26580 MW; 3E945D79 CRC32;

Query Match 76.2%; Score 48; DB 9; Length 248;
Best Local Similarity 44.4%; Pred. No. 8.60e-01;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

DB 125 AVNOYOLMO 133
QY 1 SVSEIQLMH 9

Search completed: Thu Jul 30 09:59:02 1998
Job time : 16 secs.
```

M O S E R

(TW)

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Msrch_p protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:02:44 1998; Maspar time 2.60 Seconds
47.195 Million cell updates/sec

Title: >US-08-817-547A-3
Description: (1-8) from US08817547A.pep
Perfect Score: 54
Sequence: 1 SVSEIQLM 8

Scoring table: PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq3-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 14.998; Variance 50.414; scale 0.298

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description	Pred. No.
1	54	100.0	17 18 R94192	Human parathyroid hor	2.22e+01
2	54	100.0	34 20 R99978	Human parathyroid hor	2.22e+01
3	54	100.0	34 20 W01610	Parathyroid hormone a	2.22e+01
4	54	100.0	34 7 R43361	Human parathyroid hor	2.22e+01
5	54	100.0	34 7 R43360	Human parathyroid hor	2.22e+01
6	54	100.0	34 23 W24276	Parathyroid hormone (2.22e+01
7	54	100.0	34 23 W08130	Human PTH derivative,	2.22e+01
8	54	100.0	34 23 W08131	Human PTH derivative,	2.22e+01
9	54	100.0	34 23 W24273	Wild type parathyroid	2.22e+01
10	54	100.0	34 8 R41560	[His27]hPTH (1-34).	2.22e+01
11	54	100.0	34 8 R41559	[His27]hPTH (1-34).	2.22e+01
12	54	100.0	34 22 W17954	Human parathyroid hor	2.22e+01
13	54	100.0	34 22 W17955	Human parathyroid hor	2.22e+01
14	54	100.0	34 7 R34355	Human parathyroid hor	2.22e+01
15	54	100.0	34 7 R34357	Human parathyroid hor	2.22e+01
16	54	100.0	34 18 R88829	Human parathyroid hor	2.22e+01
17	54	100.0	34 20 W14312	Cyclic parathyroid ho	2.22e+01
18	54	100.0	34 20 R99981	Porcine parathyroid h	2.22e+01
19	54	100.0	34 8 R41565	[Arg16, Gln27]hPTH (1	2.22e+01

20	54	100.0	34 8 R41552	[Glu16]hPTH (1-34).	2.22e+01
21	54	100.0	34 9 R58189	[F23,H25,H26,L27,I28,	2.22e+01
22	54	100.0	34 22 W17952	Human parathyroid hor	2.22e+01
23	54	100.0	34 7 R34368	Human parathyroid hor	2.22e+01
24	54	100.0	34 23 W08114	Human PTH derivative,	2.22e+01
25	54	100.0	34 22 W19994	Cyclised human parath	2.22e+01
26	54	100.0	34 9 R58181	[Thr33, Ala34]-hPTH(1	2.22e+01
27	54	100.0	34 7 R34367	Human parathyroid hor	2.22e+01
28	54	100.0	34 7 R34356	Human parathyroid hor	2.22e+01
29	54	100.0	34 8 R41568	[Lys15-16 His27]hPTH	2.22e+01
30	54	100.0	36 9 R58275	[Ala16]-hPTH(1-36)-NH	2.22e+01
31	54	100.0	36 9 R58276	[Met(02)18]-hPTH(1-36	2.22e+01
32	54	100.0	36 9 R58238	[D-Asp30]-hPTH(1-36)-	2.22e+01
33	54	100.0	36 9 R58237	[NMePhe34]-hPTH(1-36)-	2.22e+01
34	54	100.0	36 9 R58249	[D-Ser1]-hPTH(1-36)-N	2.22e+01
35	54	100.0	36 9 R58188	[Phe23]-hPTH(1-36)-NH	2.22e+01
36	54	100.0	37 9 R58245	[Pro0]-hPTH(1-36)-NH2	2.22e+01
37	54	100.0	38 9 R58097	[Thr13]-hPTH(1-38)-OH	2.22e+01
38	54	100.0	38 9 R58143	[Gln21]-hPTH(1-38)-OH	2.22e+01
39	54	100.0	38 9 R58114	[Val115]-hPTH(1-38)-OH	2.22e+01
40	54	100.0	44 26 P30015	Human parathyroid hor	2.22e+01
41	54	100.0	47 25 W21946	Fusion protein compri	2.22e+01
42	54	100.0	84 27 W25687	Human parathyroid hor	2.22e+01
43	54	100.0	84 8 R42076	Stability-enhanced hu	2.22e+01
44	54	100.0	84 25 W29420	Human parathyroid hor	2.22e+01
45	54	100.0	84 4 R23500	Porcine parathyroid h	2.22e+01

ALIGNMENTS

RESULT 1
ID R94192 standard; peptide; 17 AA.
AC R94192;
DE 07-OCF-1996 (first entry)
DT Human parathyroid hormone amino acids 1-17.
KW Chitosan; squid; chitin; human parathyroid hormone; hPTH; vaccine;
KM Immune response; biodegradable; synthesis method; support.
OS Synthetic.
PN CA2126132-A.
PD 18-DEC-1995.
PE 17-JUN-1994; 126132.
PF 17-JUN-1994; CA-126132.
PI (NEUG.) NEUGEBAUER W.
PI Brzelski R, Neugebauer W, Willick GE;
DR WPI; 96-151747/16.
PT Peptide synthesis by sequentially attaching desired amino acids to
PT chitosan support - the peptide-chitosan complexes are useful in
PT generating predictable and controlled immune response
PS Example 4; Page 14; 24pp; English.
CC R94191 is a peptide corresp. to amino acids 44-68 of human parathyroid
CC hormone (hPTH) that was synthesised on a chitosan support. Chitosan
CC is derived from chitin by deacetylation, the chitosan used for the
CC support was derived from squid pen chitin. Bifunctional cleavable
CC linker molecules are attached to the free amino groups of chitosan
CC and the amino acids for the protein to be synthesised are attached
CC via the linker molecules. Peptide-chitosan complexes can be used
CC directly for injection into an animal to raise an immune response as
CC chitosan is biodegradable and exhibits little or no antigenic
CC properties. The linker molecule has a third functional gp. to which
CC an immunostimulatory structure may be attached. The method may further
CC comprise capping any remaining free amino gps. on the chitosan after
CC the first amino acid and/or linker molecule has been attached.
SQ Sequence 17 AA;

Query Match 100.0%; Score 54; DB 18; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.22e+01; Mismatches 0; Indels 0; Gaps 0;

Db 1 svseiqm 8
1 |||||
QY 1 SVSEIQLM 8

RESULT 2

ID R99978 standard; peptide: 34 AA.

AC R99978;

DT 30-APR-1997 (first entry)

DE Human parathyroid hormone peptide fragment (1-34).

KW cyclic parathyroid hormone fragment; calcium-regulating activity;

KW osteoporosis; inhibit proliferation; epidermal cell; psoriasis;

KW improved half life; calcium retention; bone.

OS Synthetic.

PN DE19508672-A1.

PD 12-SEP-1996.

PF 10-MAR-1995; 008672.

PR 10-MAR-1995; DE-008672.

PA (BOE) BOEHRINGER MANNHEIM GMBH.

PI Dony C, Esswein A, Hoffmann E, Honold K, Schaefer W;

DR MPI; 96-413519/42.

PT Cyclic parathyroid hormone fragments with lactam bridge - have good

in vivo half life and are useful for treating osteoporosis and

preventing epidermal cell proliferation

Disclosure; Page 9; 14pp; German.

New cyclic parathyroid hormone fragments (CPTH) have the amino acid

sequence of h, b, p, r or CPTH(1-34), opt. extended by up to 4 amino

acids (aa) at the C-terminus and opt. shortened by up to 3 amino acids at

the N-terminus, and are cyclised between positions 13 and 17. One of

these positions is occupied by L- or D- Orn or Lys, and the other by L-

or D- Glu or Asp. CPTH have calcium-regulating activity (esp. for

treating osteoporosis and inhibit proliferation of epidermal cells (for

treating psoriasis). The CPTH have an improved half life in vivo than

known PTH fragments, increased mitogenicity and DNA-synthesising

capacity, reduced catabolic, calcium-mobilising activity and increased

activity for calcium retention and incorporation into bone. The

present sequence is that of human PTH peptide fragment (1-34).

CC present sequence is that of human PTH peptide fragment (1-34).

CC present sequence is that of human PTH peptide fragment (1-34).

CC present sequence is that of human PTH peptide fragment (1-34).

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CC present sequence is that of human PTH peptide fragment (1-34).

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CC present sequence is that of human PTH peptide fragment (1-34).

CC present sequence is that of human PTH peptide fragment (1-34).

Search completed: Thu Jul 30 10:03:01 1998
 Job time : 17 secs.

Query Match 100.0%; Score 54; DB 20; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.22e+01;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 svseidlm 8
 QY 1 svseidlm 8

Thu Jul 30 13:38:11 1998

US-08-817-547A-3.rpt

17-28 #region helix (right hand alpha)
SUMMARY #length 37 #molecular-weight 4401 #checksum 3791

Query Match 100.0%; Score 54; DB 5; length 37;
Best Local Similarity 100.0%; Pred. No. 6.75e-02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

Db 1 SVSEIQLM 8
|||
QY 1 SVSEIQLM 8

Search completed: Thu Jul 30 10:02:26 1998
Job time : 28 secs.

W E S T E R N
(TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 10:00:33 1998; MasPar time 2.09 Seconds
Abular output not generated. 95.854 Million cell updates/sec

Title: >US-08-817-547A-3
Description: (1-8) from US08817547A.pep
Perfect Score: 54
Sequence: 1 SVSEIQLM 8

Scoring table:
PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 21.952; Variance 19.669; scale 1.116

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	54	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	4.02e-03
2	54	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	4.02e-03
3	52	96.3	115	1	PTHY_RAT PARATHYROID HORMONE PR	1.58e-02
4	49	90.7	119	1	PTHY_CHICK PARATHYROID HORMONE PR	1.16e-01
5	47	87.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	4.17e-01
6	45	83.3	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	1.45e+00
7	43	79.6	1134	1	TYROSINE-PROTEIN KINAS	4.80e+00
8	43	79.6	1134	1	TYROSINE-PROTEIN KINAS	4.80e+00
9	41	75.9	259	1	Y224_METUA HYPOTHETICAL PROTEIN M	1.52e+01
10	41	75.9	312	1	Y085_MYCPN HYPOTHETICAL PROTEIN M	1.52e+01
11	41	75.9	369	1	PROB_CORGL GLUTAMATE 5-KINASE (EC	1.52e+01
12	41	75.9	441	1	CG22_ANTMA G2/MITOTIC-SPECIFIC CY	1.52e+01
13	41	75.9	481	1	KRCB_RAT RAC-BETA SERINE/THREON	1.52e+01
14	41	75.9	481	1	KRCB_HUMAN RAC-BETA SERINE/THREON	1.52e+01
15	41	75.9	591	1	FLOI_HUMAN PLACENTAL FOLATE TRANS	1.52e+01
16	41	75.9	605	1	VEL_HPYO9 REPLICATION PROTEIN E1	1.52e+01
17	41	75.9	675	1	VPS5_YEAST VACUOLAR PROTEIN SORTI	1.52e+01
18	41	75.9	835	1	VIRL_ACR76 LIMITED HOST RANGE (LH	1.52e+01
19	41	75.9	896	1	APCE_SYN4 PHYCOBILISOME 100.5 KD	1.52e+01
20	40	74.1	306	1	RIR2_VYVD RIBONUCLEOSIDE-DIPHOS	2.66e+01
21	40	74.1	341	1	YSX3_CAELD HYPOTHETICAL 39.0 KD P	2.66e+01
22	40	74.1	870	1	COPG_CAELD PROBABLE COATOWER GAMW	2.66e+01
23	40	74.1	1061	1	TRC4_ECOLI DNA PRIMASE TRAC (EC 2	2.66e+01

RESULT	ID	PTHY_HUMAN	STANDARD;	PRT;	115 AA.	ALIGNMENTS
AC	24	40	74.1	1150	1	YIC6_YEAST HYPOTHETICAL 133.0 KD
DT	25	40	74.1	1487	1	MD53_YEAST MD53 PROTEIN (MCK1 DOS
DT	26	40	74.1	3124	1	CAIC_CHICK COLLAGEN ALPHA 1(XII)
DT	27	39	72.2	106	1	RPE_RHOCA RIBULOSE-PHOSPHATE 3-E
DT	28	39	72.2	207	1	R44_CHLEL CHLOROPLAST 30S RIBOSO
DT	29	39	72.2	220	1	GTIC2_RAT GLUTATHIONE S-TRANSFER
DT	30	39	72.2	248	1	LEP3_BACSU TYPE 4 PREPILIN-LIKE P
DT	31	39	72.2	455	1	DCOR_CRIGR ORNITHINE DECARBOXYLAS
DT	32	39	72.2	455	1	DCOR_CRIGR PROLYL-TRNA SYNTHETASE
DT	33	39	72.2	461	1	DCOR_MUSPA ORNITHINE DECARBOXYLAS
DT	34	39	72.2	461	1	DCOR_MOUSE ORNITHINE DECARBOXYLAS
DT	35	39	72.2	474	1	MEC3_YEAST CHECKPOINT PROTEIN MEC
DT	36	39	72.2	503	1	HSP1_MOUSE HEAT SHOCK FACTOR PROT
DT	37	39	72.2	525	1	SP1_RARFA SERINE PROTEASE I PREC
DT	38	39	72.2	529	1	HSP1_HUMAN HEAT SHOCK FACTOR PROT
DT	39	39	72.2	567	1	CYPC_BACSU TRANSPORT ATP-BINDING
DT	40	39	72.2	626	1	TESTIS-SPECIFIC PROTEIN
DT	41	39	72.2	628	1	TESTIS-SPECIFIC PROTEIN
DT	42	39	72.2	1116	1	PROB_HETCA DNA-DIRECTED RNA POLYM
DT	43	39	72.2	1436	1	WC11_BOVIN ANTIGEN WC1.1.
DT	44	39	72.2	1827	1	CUT1_SCHPO CUT1 PROTEIN.
DT	45	39	72.2	2109	1	RRLP_VSVSJ RNA POLYMERASE BETA SU
DT	AC	21-JUL-1986	(REL. 01, CREATED)			
DT	DT	13-AUG-1987	(REL. 05, LAST SEQUENCE UPDATE)			
DT	DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)			
DT	DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).				
DT	GN	PTH.				
DT	OS	HOMO SAPIENS (HUMAN).				
DT	OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
DT	OC	EUROTHERIA; PRIMATES.				
DT	RN	[1]				
DT	RP	SEQUENCE FROM N.A.				
DT	RP	MEDLINE; 82150870.				
DT	RA	HENDY G.N., KRONENBERG H.M., POTTS J.T., JR., RICH A.;				
DT	RL	PROC. NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).				
DT	RN	[2]				
DT	RP	SEQUENCE FROM N.A.				
DT	RP	MEDLINE; 83169834.				
DT	RA	VASICER T.J., MCCREYTT B.E., FREEMAN M.W., FENNICK B.J.,				
DT	RA	HENDY G.N., POTTS J.T., JR., RICH A., KRONENBERG H.M.;				
DT	RL	PROC. NATL. ACAD. SCI. U.S.A. 80:2127-2131(1983).				
DT	RN	[3]				
DT	RP	SEQUENCE OF 26-37.				
DT	RA	JACOBS J.W., KEMPER B., NIALH H.D., HABENER J.F., POTTS J.T., JR.;				
DT	RL	NATURE 249:155-157(1974).				
DT	RN	[4]				
DT	RP	SEQUENCE OF 32-68.				
DT	RA	MEDLINE; 74111656.				
DT	RA	NIALH H.D., SAUER R.T., JACOBS J.W., KEUTMANN H.T., SEGRE G.V.,				
DT	RA	O'RIORDAN J.L.H., AUBACH G.D., POTTS J.T., JR.;				
DT	RL	PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).				
DT	RN	[5]				
DT	RP	SEQUENCE OF 61-83 AND 84-115.				
DT	RA	MEDLINE; 79082855.				
DT	RA	KEUTMANN H.T., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.,				
DT	RA	POTTS J.T., JR.;				
DT	RL	BIOCHEMISTRY 17:5723-5729(1978).				
DT	RN	[6]				
DT	RP	SEQUENCE OF 75-100.				
DT	RA	KEUTMANN H.T., NIALH H.D., JACOBS J.W., BARLING P.M., HENDY G.N.,				
DT	RA	O'RIORDAN J.L.H., POTTS J.T., JR.;				
DT	RL	(IN) CALCULUM-REGULATING HORMONES, TALMADGE R.V., OWEN M.,				
DT	RL	PARSONS J.A., EDS., PP. 9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM,				
DT	RL	(1975).				
DT	RN	[7]				

[W] [O] [S] [E] [R] [V] [H]

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:15:09 1998; MasPar time 2.61 Seconds
Tabular output not generated. 52.810 Million cell updates/sec

Title: >US-08-817-547A-32
Description: (1-9) from US08817547A.pep
Perfect Score: 68
Sequence: 1 LRKKLDVH 9

Scoring table:
PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseg31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 16.984; Variance 56.277; scale 0.302
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	68	100.0	28	4	R22072 Modified [D-Trp-12,Tyr	1.66e+00
2	68	100.0	34	26	R62432 Accelerator peptide b	1.66e+00
3	68	100.0	34	9	R58079 [L8, H10, Q18, R22, T33, A	1.66e+00
4	68	100.0	34	9	R58081 [L8, E10, Q18, R22, T33, A	1.66e+00
5	68	100.0	34	9	R58049 [L8, D10, K11, Q16, D17, L	1.66e+00
6	68	100.0	34	9	R58048 [L8, Q16, R22, T33, A34]-	1.66e+00
7	68	100.0	34	9	R58291 [Lys(For)26, Lys(For)	1.66e+00
8	68	100.0	34	9	R49697 Sequence of variant o	1.66e+00
9	68	100.0	34	22	W20002 Cyclised rat parathyr	1.66e+00
10	68	100.0	34	22	W20003 Cyclised [Nle 8,18, T	1.66e+00
11	68	100.0	35	14	W17962 Human PTH analogue [C	1.66e+00
12	68	100.0	35	14	R74516 Parathyroid hormone p	1.66e+00
13	68	100.0	35	14	R74457 Parathyroid hormone p	1.66e+00
14	68	100.0	36	9	R58275 [Ala16]-hPTH(1-36)-NH	1.66e+00
15	68	100.0	36	9	R58249 [D-Ser1]-hPTH(1-36)-NH	1.66e+00
16	68	100.0	36	9	R58285 [Ala23]-hPTH(1-36)-NH	1.66e+00
17	68	100.0	36	9	R58069 Isopropyl-[L8, K(Isopr	1.66e+00
18	68	100.0	36	9	R58026 N-alpha-methyl[Ala1]	1.66e+00

RESULT	ID	Score	Query Match	Length	DB ID	Description	Pred. No.
20	68	100.0	36	9	R58238 [D-Asp30]-hPTH(1-36)-	1.66e+00	
21	68	100.0	36	9	R58237 [NlePhe34]-hPTH(1-36)	1.66e+00	
22	68	100.0	38	9	R58028 [Thr1]-hPTH(1-38)-OH,	1.66e+00	
23	68	100.0	44	26	P30015 Human parathyroid hor	1.66e+00	
24	68	100.0	84	27	W25687 Human parathyroid hor	1.66e+00	
25	68	100.0	84	27	W21257 Human parathyroid hor	1.66e+00	
26	68	100.0	84	4	R23496 Porcine parathyroid h	1.66e+00	
27	68	100.0	84	4	R21237 Human parathyroid hor	1.66e+00	
28	68	100.0	84	4	R23380 Bovine parathyroid hor	1.66e+00	
29	68	100.0	84	4	R23241 Human parathyroid hor	1.66e+00	
30	68	100.0	84	4	R23242 Human parathyroid hor	1.66e+00	
31	68	100.0	84	4	R23356 Bovine parathyroid ho	1.66e+00	
32	68	100.0	84	4	R23357 Bovine parathyroid ho	1.66e+00	
33	68	100.0	84	4	R23243 Human parathyroid hor	1.66e+00	
34	68	100.0	84	4	R23519 Bovine parathyroid ho	1.66e+00	
35	68	100.0	84	4	R23521 Bovine parathyroid ho	1.66e+00	
36	68	100.0	84	4	R23453 Porcine parathyroid h	1.66e+00	
37	68	100.0	84	4	R21185 Human parathyroid hor	1.66e+00	
38	68	100.0	84	4	R23368 Bovine parathyroid ho	1.66e+00	
39	68	100.0	84	4	R21256 Human parathyroid hor	1.66e+00	
40	68	100.0	84	4	R21205 Human parathyroid hor	1.66e+00	
41	68	100.0	84	4	R21204 Human parathyroid hor	1.66e+00	
42	68	100.0	84	4	R21177 Human parathyroid hor	1.66e+00	
43	68	100.0	84	4	R21176 Human parathyroid hor	1.66e+00	
44	68	100.0	84	4	R21239 Human parathyroid hor	1.66e+00	
45	68	100.0	84	4	R23245 Human parathyroid hor	1.66e+00	

ALIGNMENTS

RESULT 1
ID R22072 standard; Protein; 28 AA.
AC R22072:
DE 14-JUL-1992 (first entry)
Modified [D-Trp-12,Tyr-34]PTH(7-34)NH2.
KW Parathyroid hormone; analogue; osteoporosis; hyperthyroidism;
OS tumours; hypercalcaemia; renal failure; rat.
FH Synthetic.
FH Key Location/Qualifiers
FT modified_site 7 /label= OTHER
FT /note= "OTHER - see comments"
FT modified_site 28 /label= NH2
FT modified_site 28 /label= NH2
PN US5093233-A.
PD 03-MAR-1992.
PR 25-APR-1990; 514394.
PR 25-APR-1990; US-514394.
PA (MERT) MERCK & CO INC.
PI Rosenblatt M, Roubini E, Chorev M, Nutt RF;
DR WPI; 92-096233/12.
PT New parathyroid hormone analogues - useful for treatment and in
vitro diagnosis of PTH-dependent tumours, immune disorders, and
osteoporosis and hyperparathyroidism.
PS Claim 1; Column 10; 6pp; English.
CC The peptide is modified at Lys13 (of the parent PTH) in the epsilon
amino acid gp. by N,N-disubutyl or 3-phenylpropanoyl. The
desamino form is also claimed. The PTH analogue binds with high
affinity to the peptide hormone receptor without activating the 2nd
messenger mol. The modification of the Lys residue stabilises the
bioactive conformation of PTH to enhance the activity. The peptide
may be used in vitro bioassays to measure naturally occurring
PTH and to diagnose the etiology of or to treat osteoporosis or
hypercalcaemia. It may also be used to treat hyperthyroidism and
diseases caused by aberrant proth. of hormone-like substances,
such as tumours. It may also be used to treat immune diseases such
as inflammation. It is prepd. by solid phase synthesis.
CC See also R22058-75.
SQ Sequence 28 AA:
Query Match 100.0%; Score 68; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.66e+00;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 18 lrkklqdvh 26
 QY 1 LRRKLDVH 9

RESULT 2






ID R62432 standard; peptide; 34 AA.
 AC R62432:
 DT 31-JUL-1995 (first entry)
 DE Accelerator peptide basic region peptide, P-8.
 KW Accelerator; basic amino acid; cell growth factor; gingiva;
 KW periodontal tissue; regeneration; periodontitis; periodontal pocket;
 OS down growth; epithelium; fibre adhesion; cement.
 OS Synthetic.
 PN J06234653-A.
 PD 23-AUG-1994.
 PF 10-FEB-1993; 045998.
 PR 10-FEB-1993; JP-045998.
 (SUNZ) SUNSTAR CHEM IND CO LTD.
 WPI; 95-157631/21.
 Accelerator for regenerating periodontal tissue - comprises
 PT peptide having 3-34 aminoacid residues having connected basic
 PT aminoacid residues
 PS Disclosure: Page 3: 7pp. Japanese.
 CC The sequences in R62423-36 are peptide fragments of an accelerator
 CC protein which contain at least two basic amino acids. The accelerator
 CC also comprises a cell growth factor. The accelerator may be used to
 CC accelerate the growth of periodontal tissue regeneration. The
 CC accelerator is applied by opening the gingiva, treating the tissue
 CC destroyed by periodontitis and applying the accelerator in the
 CC periodontal pocket. The accelerator reduces the down growth of the
 CC epithelium and accelerates fibre adhesion and regenerates cement.
 SQ Sequence 34 AA;

Query Match

Best Local Similarity 100.0%; Score 68; DB 26; Length 34;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 lrkklqdvh 32
 QY 1 LRRKLDVH 9

Search completed: Thu Jul 30 11:15:26 1998
 Job time : 17 secs.

```

Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
n on: Thu Jul 30 11:14:22 1998; MasPar time 3.17 Seconds
103.833 Million cell updates/sec
Tabular output not generated.

```

```

Title: >US-08-817-547A-32
Description: (1-9) from US08817547A.pep
Perfect Score: 68
Sequence: 1 LRRKKQDVH 9

Scoring table:
PAM 150
Gap 15

```

```
Searched:      120441 seqs, 36531193 residues
Post-processing: Minimum Match 0%
                Listing first 45 summaries
```

```
Database:      plr56
               1:plr1 2:plr2 3:plr3 4:plr4 5:nr13d
```

Statistics: Mean 23.542; Variance 35.708; scale 0.6559

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Full No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	68	100.0	34	5	1ZMG	parathyroid hormone 4	1.61e-020
2	68	100.0	34	5	1ZMF	parathyroid hormone 4	1.61e-020
3	68	100.0	34	5	1HTH	cyclic parathyroid ho	1.61e-020
4	68	100.0	34	5	1ZME	parathyroid hormone (1.61e-020
5	68	100.0	34	5	1ZMA	parathyroid hormone (1.61e-020
6	68	100.0	35	5	1ZMD	parathyroid hormone (1.61e-020
7	68	100.0	35	5	1ZMB	parathyroid hormone (1.61e-020
8	68	100.0	37	5	1ZRH	parathyroid hormone (1.61e-020
9	68	100.0	37	5	1ZWC	parathyroid hormone (1.61e-020
10	68	100.0	115	1	PTPG	parathyroid hormone p	1.61e-020
11	68	100.0	115	1	PTBO	parathyroid hormone p	1.61e-020
12	68	100.0	115	1	JC4202	parathyroid hormone -	1.61e-020
13	68	100.0	115	1	PTHU	parathyroid hormone p	1.61e-020
14	68	100.0	115	2	A05091	parathyroid hormone p	1.61e-020
15	58	85.3	105	2	I51851	parathyroid hormone p	1.26e+000
16	54	79.4	119	2	A34937	parathyroid hormone p	6.51e+000
17	54	79.4	421	5	1SRFA	Seryl--trna synthetase	6.51e+000
18	54	79.4	421	5	S38948	serine--trna ligase (6.51e+000
19	54	79.4	421	5	1SRFA	Seryl--trna synthetase	6.51e+000
20	54	79.4	421	5	1SERB	Seryl--trna synthetase	6.51e+000
21	54	79.4	421	5	1SERB	Seryl--trna synthetase	6.51e+000
22	54	79.4	421	5	1SESA	Seryl--trna synthetase	6.51e+000
23	54	79.4	421	5	1SESB	Seryl--trna synthetase	6.51e+000

45	54	19.4	421	5	ISERB	seryl-tRNA synthetase	6.5e+00
24	53	77.9	348	2	S45890	ODPI protein - yeast	9.70e+00
25	52	76.5	878	2	S20486	paramyosin - fruit fl	1.44e+01
26	52	76.5	879	2	S22028	paramyosin, standard	1.44e+01
27	52	76.5	2475	2	S53307	polyprotein pP220 pre	1.44e+01
28	52	76.5	257	2	S53306	floral homeotic prote	2.13e+01
29	51	75.0	317	2	S45708	MSH receptor - bovine	2.13e+01
30	51	75.0	317	2	S45707	chromosome segregation	2.13e+01
31	51	75.0	1200	2	S75524	myosin heavy chain, C	3.12e+01
32	50	73.5	412	2	S07537	tetrahydrofolylpolygl	3.12e+01
33	50	73.5	437	2	CG4113	MG397 homolog D02-Cat	3.12e+01
34	50	73.5	569	2	S62851	K12H4.1 protein - oar	3.12e+01
35	50	73.5	586	2	S44850	myosin heavy chain -	3.12e+01
36	50	73.5	621	2	S05450	smooth muscle myosin	3.12e+01
37	50	73.5	1938	2	JC5421	smooth muscle myosin	3.12e+01
38	50	73.5	1972	2	JC5430	smooth muscle myosin	3.12e+01
39	50	73.5	4723	2	A44357	dynein heavy chain, C	4.57e+01
40	49	72.1	215	2	S35640	hypothetical protein	4.57e+01
41	49	72.1	630	2	CG3432	hypothetical protein	6.64e+01
42	48	70.6	154	2	S33242	hypothetical protein	6.64e+01
43	48	70.6	229	2	GT0073	two-component respons	6.64e+01
44	48	70.6	444	2	S09681	citrate transport pro	6.64e+01
45	48	70.6	1126	2	S04716	DNA-directed RNA poly	6.64e+01

ALIGNMENTS

```

RESULT      1
ENTRY
TITLE      1ZMG      #type complete
              parathyroid hormone 4-37 mutant N-TERMINAL SUCCINYLATED -
ALTERNATE_NAMES
PDB_TITLE  n-succinyl-hPTH(4-37)
ORGANISM   succinyl human parathyroid hormone 4-37, NMR, 10 structures
REFERENCE  #formal_name synthetic
A67743
Roesch, P.; Marx, U.C.
#authors
#submission submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references PDB:1ZMG
REFERENCE  TN003319
#book
#authors
#book
In Strukturen Verschiedener Parathormonfragmente in Loesung,
pp.0, Bayreuth : University of Bayreuth (Thesis), 1996
COMMENT     Resolution: not applicable
KEYWORDS    Determination: NMR
FEATURE     disease mutation: hormone; signal
2-9
15-25
SUMMARY     #region helix (right hand alpha)\
              #region helix (right hand alpha)
              #length 34 #molecular-weight 4128 #checksum 5508

Query Match      100.0%: Score 68; DB 5; Length 34;
Best Local Similarity 100.0%: Pred. NO. 1.6E-02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      21 LRRKLDQVH 29
      |||||
OY      1 LRRKLDQVH 9

RESULT      2
ENTRY
TITLE      1ZMF      #type complete
              parathyroid hormone 4-37 mutant N-TERMINAL ACETYLATED -
ALTERNATE_NAMES
PDB_TITLE  n-acetyl-hPTH(4-37)
ORGANISM   structure of n-terminal acetylated human parathyroid hormone
REFERENCE  NMR, 10 structures
#formal_name synthetic
A67742
Roesch, P.; Marx, U.C.
#authors
#submission submitted to the Brookhaven Protein Data Bank, June 1996
#cross-references PDB:1ZMF
REFERENCE  TN003318
#book
#authors
#book
In Strukturen Verschiedener Parathormonfragmente in Loesung,

```

COMMENT PP 0, Bayreuth : University of Bayreuth (Thesis), 1996
 COMMENT Resolution: not applicable
 KEYWORDS Determination: NMR
 FEATURE disease mutation; hormone; signal
 3-6
 14-27 #region helix (right hand alpha) \
 SUMMARY #region helix (right hand alpha) \
 #length 34 #molecular-weight 4128 #checksum 5508
 Query Match 100.0%; Score 68; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.61e-02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 21 LRRKLQDVH 29
 0y 1 LRRKLQDVH 9

Search completed: Thu Jul 30 11:14:51 1998
 Time : 29 secs.

W O R L D
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:13:17 1998; MasPar time 2.13 Seconds
Tabular output not generated. 105.752 Million cell updates/sec

Title: >US-08-817-547A-32
Description: (1-9) from US08817547A.pep
Perfect Score: 68
Sequence: 1 LRRKLDVH 9

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 24.742; Variance 29.653; scale 0.834

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	68	100.0	115	1	PTHX_BOVIN PARATHYROID HORMONE PR	8.13e-04
2	68	100.0	115	1	PTHX_BOVIN PARATHYROID HORMONE PR	8.13e-04
3	68	100.0	115	1	PTHX_CANFA PARATHYROID HORMONE PR	8.13e-04
4	68	100.0	115	1	PTHX_PIG PARATHYROID HORMONE PR	8.13e-04
5	68	100.0	115	1	PTHX_RAT PARATHYROID HORMONE PR	8.13e-04
6	68	100.0	115	1	PTHX_HUMAN PARATHYROID HORMONE PR	8.13e-04
7	54	79.4	119	1	PTHX_CHICK PARATHYROID HORMONE PR	1.19e+00
8	54	79.4	119	1	PTHX_CHICK PARATHYROID HORMONE PR	1.19e+00
9	53	77.9	348	1	HM1L_YEAST HNRNP ARGININE N-METHY	1.92e+00
10	52	76.5	621	1	Y04E_YEAST HYPOTHETICAL 65.2 KD P	3.09e+00
11	52	76.5	879	1	MYSP_DROME PARAVOOSIN LONG FORM	3.09e+00
12	51	75.0	310	1	MSHR_BOVIN MELANOCYTE STIMULATING	4.92e+00
13	50	73.5	437	1	FOLC_HAEIN FOLYPOLYGLUTAMATE SYN	7.80e+00
14	50	73.5	569	1	Y397_MYCPN HYPOTHETICAL PROTEIN M	7.80e+00
15	50	73.5	586	1	YMG1_CAEEL HYPOTHETICAL 65.8 KD P	7.80e+00
16	50	73.5	4725	1	DYHC_DICDI DYNEIN HEAVY CHAIN, CY	7.80e+00
17	49	72.1	209	1	VS10_ROTBS MINOR OUTER CARSID PRO	1.23e+01
18	49	72.1	630	1	Y018_METJA HYPOTHETICAL PROTEIN M	1.23e+01
19	48	70.6	154	1	Y17K_SESV1 HYPOTHETICAL 17.8 KD P	1.92e+01
20	48	70.6	229	1	YXDL_BACSU HYPOTHETICAL 26.6 KD S	1.92e+01
21	48	70.6	360	1	H1S8_LACLA HISTIDINOL-PHOSPHATE A	1.92e+01
22	48	70.6	419	1	PEXA_PICPA PEROXISOME ASSEMBLY PR	1.92e+01
23	48	70.6	444	1	CIT1_KLEPN CITRATE-PROTON SYMPORT	1.92e+01

RESULT	ID	PTHX_BOVIN	STANDARD:	PRT:	115 AA.	ALIGNMENTS
AC	21-JUL-1986	(REL. 01, CREATED)				
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).					
GN	PTH.					
OS	BOS TAURUS (BOVINE).					
OC	EURARCTOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
OC	EUTHERIA; ARTIODACTYLA.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE: 80056617.					
RA	KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,					
RA	POTTS J.T. JR., RICH A.,					
RL	PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE: 82037785.					
RA	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;					
RA	GENE 28:319-329(1984).					
RN	[5]					
RP	SEQUENCE OF 26-115.					
RX	MEDLINE: 74142666.					
RA	HAMILTON J.W., NITAL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,					
RA	COHN D.V.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).					
RN	[6]					
RP	SEQUENCE OF 32-115.					
RX	MEDLINE: 71076162.					
RA	NITAL H.D., KEUTMANN H.T., SAUER R., HOGAN M.T., DAWSON B.F.,					
RA	AURACH G.D., POTTS J.T. JR.;					
RL	HOPPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).					
RN	[7]					
RP	SEQUENCE OF 32-115.					
RX	MEDLINE: 71063634.					

Search completed: Thu Jul 30 11:13:23 1998
Job time : 6 secs.

RA BREWER H.B. JR., RONAN R.,
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE; 71091588.
RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NITALL H.D., SAUER R.,
RA DEFOS L.J., DAWSON B.F., HOGAN M.L., AUBRACH G.D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL; V00106; G85; -.
DR EMBL; J00023; G163641; -.
DR EMBL; J00024; G163643; -.
DR EMBL; J00024; E18249; ALT_SRO.
DR EMBL; J00024; E18250; ALT_INIT.
DR EMBL; M25082; G163647; -.
DR EMBL; M25082; G163645; -.
DR PIR; A01534; PTBO.
DR PIR; A24949; A24949.
DR PROSITE; PS00335; PARATHYROID; 1.
OC HORMONE; SIGNAL.
FT SIGNAL. 1 25
FT PROPEP 26 31
FT CHAIN 32 115 PARATHYROID HORMONE.
FT CONFLICT 106 106 V -> G (IN REF. 4).
SQ SEQUENCE 115 AA; 12980 MM; 673EA5F2 CRC32;

Query Match 100.0%; Score 68; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 8.13e-04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 55 LKKKLQDVH 63
QY 1 LKKKLQDVH 9

RESULT 2
ID PTH_CANFA STANDARD; PRT; 115 AA.
AC P52212;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.
OS CANIS FAMILIARIS (DOG).
OC EUDAROTIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; CARNIVORA.
CC [1]
CC SEQUENCE FROM N.A.
CC TISSUE-PARATHYROID;
CC MEDLINE; 95369696.
RA ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,
RA DEVILLE J.W., CAPEN C.C.;
RL GENE 160:241-243(1995).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL; U15662; G55816; -.
DR PROSITE; PS00335; PARATHYROID; 1.
DR KW HORMONE; SIGNAL.
FT SIGNAL. 1 25
FT PROPEP 26 31 BY SIMILARITY.
FT CHAIN 32 115 BY SIMILARITY.
SQ SEQUENCE 115 AA; 12957 MM; 16E0DEBC CRC32;

Query Match 100.0%; Score 68; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 8.13e-04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 55 LKKKLQDVH 63
QY 1 LKKKLQDVH 9

WORLDWIDE
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mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:13:41 1998; MasPar time 3.75 Seconds
Tabular output not generated. 101.012 Million cell updates/sec

Title: >US-08-817-547A-32
Description: (1-9) from US08817547A.pep
Perfect Score: 68
Sequence: 1 LRRKLDVH 9

Scoring table: PAM 150
Gap 15

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_protein 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 23.769; Variance 29.317; scale 0.811

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	58	85.3	105	10	063473	PARATHYROID HORMONE (F	2.16e+01
2	54	79.4	735	3	017750	C06G3.9 PROTEIN	1.57e+00
3	53	77.9	398	8	004471	SIMILAR TO SACHAROMYC	2.56e+00
4	52	76.5	929	9	032491	PUTATIVE N6-ADENINE S	4.08e+00
5	52	76.5	1312	2	092878	RAD50.	4.08e+00
6	52	76.5	2475	11	008358	POLYPROTEIN PP220.	6.52e+00
7	51	75.0	242	8	P93468	MADS-BOX FAMILY TRANSC	6.52e+00
8	51	75.0	242	8	040970	PUTATIVE MADS-BOX FAMI	6.52e+00
9	51	75.0	257	8	040700	BOX PROTEIN.	6.52e+00
10	51	75.0	317	4	P79328	MELANOCYTE STIMULATING	6.52e+00
11	51	75.0	317	4	019037	MCL-R PROTEIN.	6.52e+00
12	51	75.0	733	3	024250	TARTAN PROTEIN PRECURS	6.52e+00
13	51	75.0	1200	9	P73340	CHROMOSOME SEGREGATION	6.52e+00
14	50	73.5	329	10	063338	MYOSIN HEAVY CHAIN (AA	1.04e+01
15	50	73.5	334	3	017970	CL4C10.1.	1.04e+01
16	50	73.5	621	10	063339	MYOSIN HEAVY CHAIN 21	1.04e+01
17	50	73.5	1938	10	008639	MYOSIN.	1.04e+01
18	50	73.5	1972	10	008638	MYOSIN.	1.04e+01
19	49	72.1	400	3	026648	TEKTIN B1.	1.64e+01
20	49	72.1	991	2	Q14844	MYOSIN LIGHT CHAIN KIN	1.64e+01

RESULT	ID	PRELIMINARY	PRT	105 AA.
AC	063473.			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE (FRAGMENT).			
GN	PTH.			
OS	RATTUS NORVEGICUS (RAT).			
OC	EUDAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUDAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-THYROID, AND PARATHYROID;			
RA	SCHNEIDER H.J., GROSS G., MAYER H.;			
RL	ADV. GENE TECHNOL. 21:228-229(1984).			
DR	EMBL; M54875; G601933; -.			
FT	NON_TER			
SO	SEQUENCE	105 AA;	11746 MW;	6AC3163E CRC32;

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	105 AA.
AC	063473.			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE (FRAGMENT).			
GN	PTH.			
OS	RATTUS NORVEGICUS (RAT).			
OC	EUDAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUDAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-THYROID, AND PARATHYROID;			
RA	SCHNEIDER H.J., GROSS G., MAYER H.;			
RL	ADV. GENE TECHNOL. 21:228-229(1984).			
DR	EMBL; M54875; G601933; -.			
FT	NON_TER			
SO	SEQUENCE	105 AA;	11746 MW;	6AC3163E CRC32;

Query Match 85.3%; Score 58; DB 10; Length 105;
Best Local Similarity 88.9%; Pred. No. 2.16e+01;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB	45 LRRKLDVH 53
QY	1 LRRKLDVH 9
RESULT	2
ID	017750.
AC	017750.
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE	C06G3.9 PROTEIN.
GN	C06G3.9.
OS	CANORHABDITIS ELEGANS.
OC	EUDAROTA; METAZOA; ACCELLOMATES; NEMATODA; SECCERNENTIA; RHABDITIDA.
OC	EUDAROTA; METAZOA; ACCELLOMATES; NEMATODA; SECCERNENTIA; RHABDITIDA.
RP	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-BRISTOL NZ;
RA	LATREILLE P., STELIVES L.;
RL	SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBSJ DATA BANKS.

Thu Jul 30 13:38:14 1998

US-08-817-547A-32.rsp

Page 2

DR EMBL: U61947: G1397274: -
SQ SEQUENCE 735 AA: 81001 MW: 84A565C0 CRC32:

Query Match 79.48; Score 54; DB 3; Length 735;
Best Local Similarity 66.78; Pred. No. 1.57e+00;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 486 LRRKVDIO 494
|||:|:|:

QY 1 LRRKLDVH 9

Search completed: Thu Jul 30 11:14:05 1998
Job time : 24 secs.

Db 18 LKKKIQDV 25
 |||||
 QY 1 LKKKIQDV 8

RESULT 2
 ID R62432 standard; peptide; 34 AA.

AC R62432;

DT 31-JUL-1995 (first entry)

DE Accelerator peptide basic region peptide, P-8.

KM Accelerator: basic amino acid; cell growth factor; growth; gingiva;
 KM periodontal tissue; regeneration; periodontitis; periodontal pocket;
 KM down growth; epithelium; fibre adhesion; cement.

OS Synthetic.

PN J06234653-A.

PD 23-AUG-1994.

PF 10-FEB-1993; JP-045998.

PR 10-FEB-1993; JP-045998.
 (SUNZ) SUNSTAR CHEM IND CO LTD.

WPI: 95-157631/21.

Accelerator for regenerating periodontal tissue - comprises
 peptide having 3-34 aminoacid residues having connected basic

PT aminoacid residues

PS Disclosure: Page 3; 7pp; Japanese.

CC The sequences in R62425-36 are peptide fragments of an accelerator
 protein which contain at least two basic amino acids. The accelerator

CC also comprises a cell growth factor. The accelerator may be used to
 accelerate the growth of periodontal tissue regeneration. The

CC accelerator is applied by opening the gingiva, treating the tissue
 destroyed by periodontitis and applying the accelerator in the

CC periodontal pocket. The accelerator reduces the down growth of the
 epithelium and accelerates fibre adhesion and regenerates cement.

CC Sequence 34 AA;

SQ

Query Match 100.0%; Score 59; DB 26; Length 34;
 Best Local Similarity 100.0%; Pred. No. 9.92e+00; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0;

Db 24 LKKKIQDV 31
 |||||

QY 1 LKKKIQDV 8

Search completed: Thu Jul 30 11:17:51 1998
 Job time : 15 secs.

MIRAGE

(TM)

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Masrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:16:07 1998; Maspar time 3.11 Seconds
Tabular output not generated. 93.824 Million cell updates/sec

Title: >US-08-817-547A-33
Description: (1-8) from US08817547A.dep
Perfect Score: 59
Sequence: 1 LRRKLODV 8

Scoring table: PAM 150
Gap 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr56
1:plr1 2:plr2 3:plr3 4:plr4 5:nrl3d

Statistics: Mean 22.968; Variance 34.253; scale 0.671

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Query	Match	Length	ID	Description	Pred. No.
1	59	100.0	34	parathyroid hormone 4	4.79e-01
2	59	100.0	34	parathyroid hormone 4	4.79e-01
3	59	100.0	34	parathyroid hormone 4	4.79e-01
4	59	100.0	34	parathyroid hormone 4	4.79e-01
5	59	100.0	34	parathyroid hormone 4	4.79e-01
6	59	100.0	34	parathyroid hormone 4	4.79e-01
7	59	100.0	34	parathyroid hormone 4	4.79e-01
8	59	100.0	34	parathyroid hormone 4	4.79e-01
9	59	100.0	34	parathyroid hormone 4	4.79e-01
10	59	100.0	34	parathyroid hormone 4	4.79e-01
11	59	100.0	34	parathyroid hormone 4	4.79e-01
12	59	100.0	34	parathyroid hormone 4	4.79e-01
13	59	100.0	34	parathyroid hormone 4	4.79e-01
14	59	100.0	34	parathyroid hormone 4	4.79e-01
15	59	100.0	34	parathyroid hormone 4	4.79e-01
16	59	100.0	34	parathyroid hormone 4	4.79e-01
17	59	100.0	34	parathyroid hormone 4	4.79e-01
18	59	100.0	34	parathyroid hormone 4	4.79e-01
19	59	100.0	34	parathyroid hormone 4	4.79e-01
20	59	100.0	34	parathyroid hormone 4	4.79e-01
21	59	100.0	34	parathyroid hormone 4	4.79e-01
22	59	100.0	34	parathyroid hormone 4	4.79e-01
23	59	100.0	34	parathyroid hormone 4	4.79e-01

Query	Match	Length	ID	Description	Pred. No.
1	59	100.0	34	parathyroid hormone 4	4.79e-01
2	59	100.0	34	parathyroid hormone 4	4.79e-01
3	59	100.0	34	parathyroid hormone 4	4.79e-01
4	59	100.0	34	parathyroid hormone 4	4.79e-01
5	59	100.0	34	parathyroid hormone 4	4.79e-01
6	59	100.0	34	parathyroid hormone 4	4.79e-01
7	59	100.0	34	parathyroid hormone 4	4.79e-01
8	59	100.0	34	parathyroid hormone 4	4.79e-01
9	59	100.0	34	parathyroid hormone 4	4.79e-01
10	59	100.0	34	parathyroid hormone 4	4.79e-01
11	59	100.0	34	parathyroid hormone 4	4.79e-01
12	59	100.0	34	parathyroid hormone 4	4.79e-01
13	59	100.0	34	parathyroid hormone 4	4.79e-01
14	59	100.0	34	parathyroid hormone 4	4.79e-01
15	59	100.0	34	parathyroid hormone 4	4.79e-01
16	59	100.0	34	parathyroid hormone 4	4.79e-01
17	59	100.0	34	parathyroid hormone 4	4.79e-01
18	59	100.0	34	parathyroid hormone 4	4.79e-01
19	59	100.0	34	parathyroid hormone 4	4.79e-01
20	59	100.0	34	parathyroid hormone 4	4.79e-01
21	59	100.0	34	parathyroid hormone 4	4.79e-01
22	59	100.0	34	parathyroid hormone 4	4.79e-01
23	59	100.0	34	parathyroid hormone 4	4.79e-01

ALIGNMENTS

Query	Match	Length	ID	Description	Pred. No.
1	59	100.0	34	parathyroid hormone 4	4.79e-01
2	59	100.0	34	parathyroid hormone 4	4.79e-01
3	59	100.0	34	parathyroid hormone 4	4.79e-01
4	59	100.0	34	parathyroid hormone 4	4.79e-01
5	59	100.0	34	parathyroid hormone 4	4.79e-01
6	59	100.0	34	parathyroid hormone 4	4.79e-01
7	59	100.0	34	parathyroid hormone 4	4.79e-01
8	59	100.0	34	parathyroid hormone 4	4.79e-01
9	59	100.0	34	parathyroid hormone 4	4.79e-01
10	59	100.0	34	parathyroid hormone 4	4.79e-01
11	59	100.0	34	parathyroid hormone 4	4.79e-01
12	59	100.0	34	parathyroid hormone 4	4.79e-01
13	59	100.0	34	parathyroid hormone 4	4.79e-01
14	59	100.0	34	parathyroid hormone 4	4.79e-01
15	59	100.0	34	parathyroid hormone 4	4.79e-01
16	59	100.0	34	parathyroid hormone 4	4.79e-01
17	59	100.0	34	parathyroid hormone 4	4.79e-01
18	59	100.0	34	parathyroid hormone 4	4.79e-01
19	59	100.0	34	parathyroid hormone 4	4.79e-01
20	59	100.0	34	parathyroid hormone 4	4.79e-01
21	59	100.0	34	parathyroid hormone 4	4.79e-01
22	59	100.0	34	parathyroid hormone 4	4.79e-01
23	59	100.0	34	parathyroid hormone 4	4.79e-01

Thu Jul 30 13:38:15 1998

US-08-817-547A-33.rpr

Page 2

pp. 0, Bayreuth : University of Bayreuth (Thesis), 1996

COMMENT Resolution: not applicable
Determination: NMR
KEYWORDS disease mutation; hormone; signal

FEATURE
3-6 #region helix (right hand alpha)\
14-27 #region helix (right hand alpha)
#length 34 #molecular-weight 4128 #checksum 5508

SUMMARY
Query Match 100.0%; Score 59; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.79e-01;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 21 LRRKLDV 28
|||
Q7 1 LRRKLDV 8

Search completed: Thu Jul 30 11:16:30 1998
Time : 23 secs.

WISCONSIN

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:15:44 1998; Maspar time 2.11 Seconds
Tabular output not generated. 95.235 Million cell updates/sec

Title: >US-08-817-547A-33
Description: (1-8) from US08817547A.pap
Perfect Score: 59
Sequence: 1 LRRKLDV 8

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 24.101; Variance 28.427; scale 0.848

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	59	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	4.95e-02
2	59	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	4.95e-02
3	59	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	4.95e-02
4	59	100.0	115	1	PTHY_RAT PARATHYROID HORMONE PR	4.95e-02
5	59	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	4.95e-02
6	51	86.4	310	1	SYNTAXIN-RELATED PROTEIN	2.83e+00
7	51	86.4	317	1	MSHR_BOVIN MELANOCYTE STIMULATING	2.83e+00
8	50	84.7	421	1	SYS_THETH SERYL-TRNA SYNTHETASE	4.56e+00
9	50	84.7	437	1	FOLC_HAEN FOLYPOLYGLUTAMATE SYN	4.56e+00
10	50	84.7	586	1	YMG1_GABEL HYPOTHETICAL 65.8 KD P	4.56e+00
11	50	84.7	621	1	Y04E_MYCTU HYPOTHETICAL 69.2 KD P	4.56e+00
12	50	84.7	4725	1	DYHC_DICDI DYNENIN HEAVY CHAIN, CY	4.56e+00
13	49	83.1	209	1	VS10_ROTBS MINOR OUTER CAPSID, PRO	7.30e+00
14	49	83.1	630	1	Y019_METJA HYPOTHETICAL PROTEIN M	7.30e+00
15	48	81.4	154	1	Y17K_SSV1 HYPOTHETICAL 17.8 KD P	1.16e+01
16	48	81.4	419	1	PEXA_PICPA PEROXISOME ASSEMBLY PR	1.16e+01
17	48	81.4	1126	1	PROB_SRIAC DNA-DIRECTED RNA POLYM	1.16e+01
18	47	79.7	100	1	Y191_ECOLI INSERTION ELEMENT IS91	1.83e+01
19	47	79.7	112	1	Y191_SHIDY INSERTION ELEMENT IS91	1.83e+01
20	46	78.0	100	1	RRI4_PORPU CHLOROPLAST 30S RIBOSO	2.86e+01
21	46	78.0	224	1	TCID_SALTY TRANSGLUTAMINASE	2.86e+01
22	46	78.0	229	1	YXDJ_BACSU HYPOTHETICAL 26.6 KD S	2.86e+01
23	46	78.0	326	1	YIEL_YEAST 36.7 KD PROTEIN IN CBR	2.86e+01

ALIGNMENTS

RESULT ID	1	PTHY_BOVIN	STANDARD:	PRT:	115 AA.
AC	21-JUL-1986	(REL. 01, CREATED)			
AC	P01268:				
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRLN) (PTH).				
GN	PTH.				
OS	BOS TAURUS (BOVINE).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; ARTIODACTYLA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 80056617.				
RA	KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,				
RA	POTTS J.T. JR., RICH A.J.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 82037785.				
RA	WEAVER C.A., GORDON D.F., KEMPER B.;				
RA	MOUL. CELL. ENDOCRINOL. 28:411-424(1982).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 84262483.				
RA	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;				
RA	GENE 28:319-329(1984).				
RN	[5]				
RP	SEQUENCE OF 26-115.				
RX	MEDLINE: 74142666.				
RA	HAKULTON J.W., NYALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,				
RA	COHN D.V.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).				
RN	[6]				
RP	SEQUENCE OF 32-115.				
RX	MEDLINE: 71076162.				
RA	NIAL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,				
RA	AURACH G.D., POTTS J.T. JR.;				
RL	HOPPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).				
RN	[7]				
RP	SEQUENCE OF 32-115.				
RX	MEDLINE: 71063634.				

RA BREWER H.B. JR., RONAN R.;
 6600 WAT ACAD SCT U.S.A. 67:1862-1869(1970)..

RP SYNTHESIS OF 32-05.
RX MEDLINE; 71091588.

PROC. NATL. ACAD. SCI. U.S.A. 68:63-6(1971).
-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN

CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC
CC
CC

DR	EMBL;	V00100;	803;	-
DR	EMBL;	J00023;	G163641;	-
DR	EMBL;			

DR EMBL; J00024; GI53643; -;
DR EMBL; J00024; E18249; ALT_SEQ.

```
DR      EMBL; J00024; E18250; ALT_INIT.  
DR      EMBL; K01938; G163647; -.
```

EMBL; M25082; G163645; -.
PTR. A01534; PTBO.

DR PIR; A24949; A24949.
DR POSTTE: PS00335: PARATHYROID; 1.

PROBIE; E000000; 25
HORMONE; SIGNAL. 1

FT	SIGNAL	PROPEP	1	26	31	41	DATE

FT	CHAIN	32	115	PAGE
FT	CONFLICT	106	106	V ->

SEQUENCE	115 AA;	12980 MW;	6
SQ			

Query Match	100.0%;	Score
Similarity	100.0%;	Pred

Best local conservation 0;
Matches 8; Conservative 0;

Db 55 L R K K L Q D V 62

1 L R K K L Q D V 8

RESULT	2	STANDARD;	PR
--------	---	-----------	----

ID	NAME	AGE	SEX	DOB	STATUS	CREATED
AC	P52212;	01	00	00	1906	(PFI. 34. CREATED)

DT	01-OCT-1996	(REL. 34,	LAST SEQUE
DT	01-OCT-1996	(REL. 34,	LAST SEQUE

DT 01-OCT-1996 (REL. 34, LAST NAME
DE PARATHYROID HORMONE PRECURSOR (P

GN PTH.
OS CANIS FAMILIARIS (DOG).

EUKARYOTA; METAZOA; CHORDATA; VE
EUTHERIA; CARNIVORA.

CO [1]
-RN
SECURITY FROM N A

SEQUENCE FROM N-111;
TISSUE-PARATHYROID;
05360606

RA ROSOL T.J., STEINMEYER C.L., MCC

RA DEWILLE J.W., CAPEN C.C.;
RL GENE 160:241-243(1995).

CC -1- FUNCTION: PTH ELEVATES CALC
CC BONE AND PREVENTING THEIR R

EMBL; U15662; G558916; -.
PROCTER; PS00335. PARATHYROID;

DR	PROFILE; F800000;
KW	HORMONE; SIGNAL.
	1 35 BY

FT	SIGNAL	1	22
FT	PROPEP	26	31
			11
			BY
			DA

FT	CHAIN	32	115	FA
SO	SEQUENCE	115	AA;	12957 MW;

Query Match	Score
100.08;	Score

Best Local Similarity 100.0%; Pre
watched 9; Conservative 0;

Matches 8, conducted

```
Db 55 LKKKLDV 62
      |||||
```

QY 1 LKKLQDV 8

RC TISSUE-THYROID, AND PARATHYROID:
 RA SCHMELZER H.J., GROSS G., MAYER H.;
 RL ADV. GENE TECHNOL. 21:228-229(1984).
 DR EMBL; M54875; G601933; -.
 FT NON_TER 1
 SQ SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;

Query Match 88.1%; Score 52; DB 10; Length 105;
 Best local similarity 100.0%; Pred. NO. 2.21e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 45 LRKLIQD 51
 QY 1 LRKLIQD 7

Search completed: Thu Jul 30 11:17:18 1998
 Job time : 29 secs.

MIRCH
(TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:20:11 1998; Maspar time 2.56 Seconds
41.969 Million cell updates/sec
Tabular output not generated.

Title: >US-08-817-547A-34
Description: (1-7) from US08817547A.pep
Perfect Score: 52
Sequence: 1 LRKRLQD 7

Scoring table:

PAM 150
Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 15.842; Variance 50.654; scale 0.313

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	52	100.0	34 26	R62432	Accelerator peptide b	3.78e+01
2	52	100.0	34 2	R08300	Human parathyroid hor	3.78e+01
3	52	100.0	34 9	R58291	[Lys(For)26, Lys(For)	3.78e+01
4	52	100.0	34 9	R58232	[Lys32]-hPTH(1-34)-NH	3.78e+01
5	52	100.0	34 7	R34358	Human parathyroid hor	3.78e+01
6	52	100.0	34 22	W20009	Cyclised [Nle 8,18, T	3.78e+01
7	52	100.0	34 22	W20003	Cyclised [Nle 8,18, T	3.78e+01
8	52	100.0	34 22	W17963	Human PTH analogue (C	3.78e+01
9	52	100.0	35 14	R74453	Parathyroid hormone p	3.78e+01
10	52	100.0	35 14	R74486	Parathyroid hormone p	3.78e+01
11	52	100.0	35 14	R74440	Parathyroid hormone p	3.78e+01
12	52	100.0	35 14	R74439	Parathyroid hormone p	3.78e+01
13	52	100.0	35 14	R74485	Parathyroid hormone p	3.78e+01
14	52	100.0	35 14	R74397	Parathyroid hormone p	3.78e+01
15	52	100.0	36 9	R58191	[Ala34]-hPTH(1-36)-NH	3.78e+01
16	52	100.0	36 9	R58253	[4-aminobenzoic acid1	3.78e+01
17	52	100.0	36 9	R58237	[NMePhe34]-hPTH(1-36)	3.78e+01
18	52	100.0	36 9	R58238	[D-Asp30]-hPTH(1-36)-	3.78e+01
19	52	100.0	36 9	R58041	[Le,D10,K11,S14,I15,Q	3.78e+01

20	52	100.0	36 9	R58285	[Ala23]-hPTH(1-36)-NH	3.78e+01
21	52	100.0	36 9	R58069	Isopropyl- [Le,K1Isop	3.78e+01
22	52	100.0	36 9	R58227	[D-Gln29]-hPTH(1-36)-	3.78e+01
23	52	100.0	38 9	R58136	[Arg19]-hPTH(1-38)-OH	3.78e+01
24	52	100.0	38 9	R58108	[Arg14]-hPTH(1-38)-OH	3.78e+01
25	52	100.0	44 26	P30015	Human parathyroid hor	3.78e+01
26	52	100.0	44 27	W25687	Human parathyroid hor	3.78e+01
27	52	100.0	84 4	R23356	Bovine parathyroid ho	3.78e+01
28	52	100.0	84 4	R23357	Bovine parathyroid ho	3.78e+01
29	52	100.0	84 4	R23241	Human parathyroid hor	3.78e+01
30	52	100.0	84 4	R23242	Human parathyroid hor	3.78e+01
31	52	100.0	84 4	R23521	Bovine parathyroid ho	3.78e+01
32	52	100.0	84 4	R23453	Porcine parathyroid h	3.78e+01
33	52	100.0	84 4	R23243	Human parathyroid hor	3.78e+01
34	52	100.0	84 4	R23519	Bovine parathyroid hor	3.78e+01
35	52	100.0	84 4	R23434	Porcine parathyroid h	3.78e+01
36	52	100.0	84 4	R23273	Bovine parathyroid ho	3.78e+01
37	52	100.0	84 4	R21256	Human parathyroid hor	3.78e+01
38	52	100.0	84 4	R23368	Bovine parathyroid ho	3.78e+01
39	52	100.0	84 4	R23256	Bovine parathyroid ho	3.78e+01
40	52	100.0	84 4	R21251	Human parathyroid hor	3.78e+01
41	52	100.0	84 4	R23522	Human parathyroid hor	3.78e+01
42	52	100.0	84 4	R23547	Bovine parathyroid ho	3.78e+01
43	52	100.0	84 7	R24335	Bovine parathyroid ho	3.78e+01
44	52	100.0	84 4	R21239	Human parathyroid hor	3.78e+01
45	52	100.0	84 4	R23245	Human parathyroid hor	3.78e+01

ALIGNMENTS

RESULT 1
ID R62432 standard; peptide; 34 AA.
AC R62432;
DT 31-JUL-1995 (first entry)
DE Accelerator peptide basic region peptide, p-8.
KW Accelerator; basic amino acid; cell growth factor; growth; gingiva;
KW Periodontal tissue; regeneration; periodontitis; periodontal pocket;
KW down growth; epithelium; fibre adhesion; cement.
OS Synthetic.
PN J06234653-A.
PD 23-AUG-1994.
PF 10-FEB-1993; 045998.
PR 10-FEB-1993; JP-045998.
PA (SUNZ) SUNSTAR CHEM IND CO LTD.
DR WPI; 95-157631/21.
PT Accelerator for regenerating periodontal tissue - comprises
PT peptide having 3-34 aminoacid residues having connected basic
PT aminoacid residues.
PS Disclosure; Page 3; 7pp; Japanese.
CC The sequences in R62425-36 are peptide fragments of an accelerator
CC protein which contain at least two basic amino acids. The accelerator
CC also comprises a cell growth factor. The accelerator may be used to
CC accelerate the growth of periodontal tissue regeneration. The
CC accelerator is applied by opening the gingiva, treating the tissue
CC destroyed by periodontitis and applying the accelerator in the
CC periodontal pocket. The accelerator reduces the down growth of the
CC epithelium and accelerates fibre adhesion and regenerates cement.
SQ Sequence 34 AA;
Query Match 100.0%; Score 52; DB 26; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.78e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 24 lrklqgd 30
QY 1 LRKRLQD 7
RESULT 2
ID R08300 standard; protein; 34 AA.
AC R08300;
DT 18-FEB-1991 (first entry)
DE Human parathyroid hormone analogue, Tnp12 hPTH(7-34).

KW Osteoporosis; hypercalcemia; hyperparathyroidism; hypertension.
OS Homo sapiens.
PN US4968669-A.
PD 06-NOV-1990.
PF 21-APR-1989; 341597.
PR 09-MAY-1988; US-191512.
PR 21-APR-1989; US-341597.
PA (MERI) MERCK & CO INC.
PI Rosenblatt M, Chorev M;
DR WPI; 90-354642/47.
PT New para:thyroid hormone analogues - which inhibit hormone
PT activity by binding receptors while not producing second
PT messenger molecules
PS Claim 1; Column 8; 6pp; English.
CC Peptide analogues have high affinity for PTH cell surface receptors,
CC but do not stimulate production of secondary messenger molecules.
CC They may be used in inhibition of PTH action, and in diagnosis and
CC treatment of osteoporosis, hypercalcemia and hyperparathyroidism.
CC Analogues may also be used in treatment of tumours and other cells
CC overproducing peptide hormone-like substances, and immune diseases
eg. allergic inflammation and hyperactive lymphocytes.
SQ Naturally occurring PTH levels may also be measured in vitro.
Sequence 34 AA;

Query Match 100.0%; Score 52; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.78e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 24 LKKLQD 30
| | | | | | | |
QY 1 LKKKLD 7

Search completed: Thu Jul 30 11:20:26 1998
Job time : 15 secs.

MIRAGE (TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:19:28 1998; MasPar time 3.06 Seconds
Tabular output not generated. 83.440 Million cell updates/sec

Title: >US-08-817-547A-34
Description: (1-7) from US08817547A.pep
Perfect Score: 52
Sequence: 1 LRRK1QD 7

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr56
1:plr1 2:plr2 3:plr3 4:plr4 5:plr13d

Statistics: Mean 21.946; Variance 32.007; scale 0.686

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description	Pred. No.
1	52	100.0	34	5 12WG	parathyroid hormone 4	4.07e+00
2	52	100.0	34	5 12WF	parathyroid hormone 4	4.07e+00
3	52	100.0	34	5 12RH	cyclic parathyroid ho	4.07e+00
4	52	100.0	34	5 12WE	parathyroid hormone (4.07e+00
5	52	100.0	34	5 12NA	parathyroid hormone (4.07e+00
6	52	100.0	35	5 12WD	parathyroid hormone (4.07e+00
7	52	100.0	36	5 12WB	parathyroid hormone (4.07e+00
8	52	100.0	37	5 12WB	parathyroid hormone (4.07e+00
9	52	100.0	37	5 12WB	parathyroid hormone (4.07e+00
10	52	100.0	105	2 151851	parathyroid hormone -	4.07e+00
11	52	100.0	115	2 J04202	parathyroid hormone	4.07e+00
12	52	100.0	115	2 A05091	parathyroid hormone	4.07e+00
13	52	100.0	115	1 PRH	parathyroid hormone p	4.07e+00
14	52	100.0	115	1 PRH	parathyroid hormone p	4.07e+00
15	52	100.0	115	1 PRH	parathyroid hormone p	4.07e+00
16	52	100.0	115	1 PRH	parathyroid hormone p	4.07e+00
17	47	90.4	133	2 S53306	floral homeotic prote	6.22e+00
18	47	90.4	133	2 S75121	hypothetical protein	3.23e+01
19	47	90.4	154	2 S03242	hypothetical protein	3.23e+01
20	46	88.5	100	2 F69342	DNA primase homolog -	3.23e+01
21	46	88.5	122	2 S56508	hypothetical 11.6K pr	4.80e+01
22	46	88.5	134	2 D70083	hypothetical protein	4.80e+01
23	46	88.5	224	2 G64750	hypothetical protein	4.80e+01
				2 A33861	Trans-activating tran	4.80e+01

24	46	88.5	447	2 B40896	Ca2+/calmodulin-depen	4.80e+01
25	46	88.5	509	2 S22339	steroid 17alpha-monoo	4.80e+01
26	46	88.5	637	1 WOEC2M	phosphotransferase sy	4.80e+01
27	46	88.5	745	2 S48019	kinesin-related prote	4.80e+01
28	46	88.5	754	2 S48020	kinesin-related prote	4.80e+01
29	46	88.5	793	2 S34830	kinesin-related prote	4.80e+01
30	46	88.5	806	2 E64221	phenylalanine-tRNA l	4.80e+01
31	46	88.5	899	2 S51341	probable membrane pro	4.80e+01
32	46	88.5	1231	2 A54803	microtubule-associate	4.80e+01
33	46	88.5	2492	1 C44213	nonstructural polypro	4.80e+01
34	46	88.5	2492	1 A44213	nonstructural polypro	4.80e+01
35	46	88.5	2492	1 MNMTD	nonstructural polypro	4.80e+01
36	46	88.5	192	2 S22577	hypothetical protein	7.11e+01
37	46	86.5	258	2 S57793	homeotic protein Ad3	7.11e+01
38	45	86.5	275	2 J05492	insertion element ISH	7.11e+01
39	45	86.5	355	2 S57398	NUVA protein - Emeric	7.11e+01
40	45	86.5	430	1 VEMSGF	glial fibrillary acid	7.11e+01
41	45	86.5	443	2 S57328	uvrH protein - Emeric	7.11e+01
42	45	86.5	477	2 S55494	CHRC4 type zinc finger	7.11e+01
43	45	86.5	957	2 C59463	type I restriction-mo	7.11e+01
44	45	86.5	1999	1 S21801	myosin heavy chain, n	7.11e+01
45	45	86.5	2475	2 S35307	polyprotein pp220 pre	7.11e+01

ALIGNMENTS

RESULT	ENTRY	TITLE	12WG	#type complete
1	12WG	parathyroid hormone 4	37	mutant N-TERMINAL SUCCINYLATED -
1	12WG	synthetic		
ALTERNATE_NAMES		n-succinyl-hph(4-37)		
PDB_TITLE		succinyl human parathyroid hormone 4-37, NMR, 10 structures		
ORGANISM		#formal_name synthetic		
REFERENCE		A67743		
#authors		Roesch, P.; Marx, U.C.		
#submission		submitted to the Brookhaven Protein Data Bank, June 1996		
#cross-references		PDB:12WG		
REFERENCE		TN003319		
#authors		Marx, U.C.		
#book		In Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996		
COMMENT		Resolution: not applicable		
COMMENT		determination: NMR		
KEYWORDS		disease mutation; hormone; signal		
FEATURE				
2-9				
15-25				
SUMMARY		#region helix (right hand alpha)\		
		#region helix (right hand alpha)		
		#length 34 #molecular-weight 4128 #checksum 5508		
Query Match		100.0%; Score 52; DB 5; Length 34;		
Best Local Similarity		100.0%; Pred. No. 4.07e+00;		
Matches		7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Db	21	LRRK1QD 27		
Qy	1	LRRK1QD 7		
RESULT	2	12WF	#type complete	
ENTRY		parathyroid hormone 4	37	mutant N-TERMINAL ACETYLATED -
TITLE		synthetic		
ALTERNATE_NAMES		n-acetyl-hph(4-37)		
PDB_TITLE		structure of n-terminal acetylated human parathyroid hormone, NMR, 10 structures		
ORGANISM		#formal_name synthetic		
REFERENCE		A67742		
#authors		Roesch, P.; Marx, U.C.		
#submission		submitted to the Brookhaven Protein Data Bank, June 1996		
#cross-references		PDB:12WF		
REFERENCE		TN003318		
#authors		Marx, U.C.		
#book		In Strukturen Verschiedener Parathormonfragmente in Loesung,		

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Page 2

pp.0, Bayreuth : University of Bayreuth (Thesis), 1996
COMMENT Resolution: not applicable
COMMENT Determination: NMR
KEYWORDS disease mutation; hormone; signal
FEATURE
3-6 #region helix (right hand alpha)\
14-27 #region helix (right hand alpha)
SUMMARY #length 34 #molecular-weight 4128 #checksum 5508
Query Match 100.0%; Score 52; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.07e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 21 LRRKLOD 27
QY 1 LRRKLOD 7

Search completed: Thu Jul 30 11:19:55 1998
Job time : 27 secs.

MUSE RELEASE

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Search_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:18:09 1998; MasPar time 2.07 Seconds
Tabular output not generated. 84.981 Million cell updates/sec

Title: >US-08-817-547A-34
Description: (1-7) from US08817547A.pep
Perfect Score: 52
Sequence: 1 LRKRLQD 7

Scoring table:
PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 23.054; Variance 26.515; scale 0.869

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	52	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	6.49e-01
2	52	100.0	115	1	PTHY_CANFA PARATHYROID HORMONE PR	6.49e-01
3	52	100.0	115	1	PTHY_PIG PARATHYROID HORMONE PR	6.49e-01
4	52	100.0	115	1	PTHY_RAT PARATHYROID HORMONE PR	6.49e-01
5	52	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	6.49e-01
6	48	92.3	621	1	Y04E_MYCTU HYPOTHETICAL 69.2 KD P	4.84e+00
7	47	90.4	154	1	Y17K_SSVL HYPOTHETICAL 17.8 KD P	7.85e+00
8	46	88.5	100	1	Y191_ECOLI INSERTION ELEMENT 1591	1.26e+01
9	46	88.5	112	1	Y191_SHIDY INSERTION ELEMENT 1591	1.26e+01
10	46	88.5	224	1	TCTD_SALTY TRANSCRIPTIONAL REGULA	1.26e+01
11	46	88.5	447	1	KCC2_YEAST CYTOCHROME P450 XITAI	1.26e+01
12	46	88.5	509	1	CPT7_PIG PTS SYSTEM, MANNITOL-S	1.26e+01
13	46	88.5	637	1	PTMA_ECOLI KINESIN-LIKE PROTEIN B	1.26e+01
14	46	88.5	745	1	KATC_ARATH KINESIN-LIKE PROTEIN B	1.26e+01
15	46	88.5	754	1	KATC_ARATH KINESIN-LIKE PROTEIN A	1.26e+01
16	46	88.5	793	1	KATA_ARATH KINESIN-LIKE PROTEIN A	1.26e+01
17	46	88.5	806	1	SYEB_MYCGE PHENYLALANYL-TRNA SYNT	1.26e+01
18	46	88.5	1231	1	KIF4_MOUSE KINESIN-LIKE PROTEIN K	1.26e+01
19	46	88.5	2492	1	POLN_EEVTY NONSTRUCTURAL POLYPROT	1.26e+01
20	46	88.5	2492	1	POLN_EEVTY NONSTRUCTURAL POLYPROT	1.26e+01
21	46	88.5	2492	1	POLN_EEVTY NONSTRUCTURAL POLYPROT	1.26e+01
22	45	86.5	229	1	YXDJ_BACSU HYPOTHETICAL 26.6 KD S	2.02e+01
23	45	86.5	428	1	GFAP_BOVIN GLIAL FIBRILLARY ACIDI	2.02e+01

Result	ID	PTHY_BOVIN	STANDARD	PRT	115 AA.
24	45	86.5	430	1	GFAP_RAT GLIAL FIBRILLARY ACIDI
25	45	86.5	430	1	GFAP_MOUSE GLIAL FIBRILLARY ACIDI
26	45	86.5	4725	1	DYHC_DICDI DYNEIN HEAVY CHAIN, CY
27	44	84.6	100	1	RRI4_PORPU CHLOROPLAST 30S RIBOSO
28	44	84.6	110	1	PTCA_BACSU PTS SYSTEM, CELLOBIOSE
29	44	84.6	182	1	Y922_HAEIN HYPOTHETICAL LIPOPROTE
30	44	84.6	310	1	SYNK_ARATH SYNTAXIN-RELATED PROTE
31	44	84.6	314	1	GCR_SHEEP GLUCOCORTICOID RECEPTO
32	44	84.6	335	1	HIS9_YEAST HISTIDINOL-PHOSPHATASE
33	44	84.6	444	1	CITI_KLEPN CITRATE-PROTON SYMPORT
34	44	84.6	450	1	VIMB_CARAU VIMENTIN BETA.
35	44	84.6	453	1	OP2_MAIZE OPAQUE-2 REGULATORY PR
36	44	84.6	458	1	IF3T_TORCA TYPE III INTERMEDIATE
37	44	84.6	461	1	VIME_ONCMY VIMENTIN.
38	44	84.6	463	1	VIM4_XENLA VIMENTIN 4.
39	44	84.6	470	1	BFRI_YEAST NUCLEAR SEGREGATION PR
40	44	84.6	565	1	NO56_SOYBN LATE NODULIN 56 (N-56)
41	44	84.6	617	1	ASMA_ECOLI ASMA PROTEIN PRECURSOR
42	44	84.6	630	1	Y019_MENTA HYPOTHETICAL PROTEIN M
43	44	84.6	669	1	YMS2_YEAST HYPOTHETICAL 76.2 KD P
44	44	84.6	752	1	HPRI_YEAST HPRI PROTEIN.
45	44	84.6	2843	1	APC_HUMAN ADENOMATOUS POLYPOSIS

ALIGNMENTS

Result	ID	PTHY_BOVIN	STANDARD	PRT	115 AA.
AC	P01268;				
DT	21-JUL-1986 (REL. 01, CREATED)				
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).				
GN	PTH.				
OS	BOS TAURUS (BOVINE).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	ETHERIA; ARTIODACTYLA.				
RN	[1]				
RA	SEQUENCE FROM N.A.				
RX	MEDLINE; 80056617.				
RA	KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,				
RA	POTTS J.T., JR., RICH A.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).				
RN	[2]				
RA	SEQUENCE FROM N.A.				
RX	MEDLINE; 82037785.				
RA	WEAVER C.A., GORDON D.F., KEMPER B.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).				
RN	[3]				
RA	SEQUENCE FROM N.A.				
RX	MEDLINE; 83105964.				
RA	WEAVER C.A., GORDON D.F., KEMPER B.;				
RL	MOL. CELL. ENDOCRINOL. 28:411-424(1982).				
RN	[4]				
RA	SEQUENCE FROM N.A.				
RX	MEDLINE; 84262483.				
RA	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;				
RL	GENE 28:319-329(1984).				
RN	[5]				
RA	SEQUENCE OF 26-115.				
RX	MEDLINE; 74142666.				
RA	HAMILTON J.W., NITALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,				
RL	COHN D.V.;				
RN	[6]				
RA	PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).				
RN	[7]				
RA	SEQUENCE OF 32-115.				
RX	MEDLINE; 71076162.				
RA	NITALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DANSON B.F.,				
RL	AURBACH G.D., POTTS J.T. JR.;				
RN	[7]				
RA	HOPPE-SEYLER S.Z. PHYSIOL. CHEM. 351:1586-1588(1970).				
RN	[7]				
RA	SEQUENCE OF 32-115.				
RX	MEDLINE; 71063634.				

Search completed: Thu Jul 30 11:18:16 1998
Job time : 7 secs.

RA BREWER H. B. JR., RONAN R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE: 71091588.
RA POTTS J.T. JR., TREGGAR G.W., KEUTMANN H.T., NIAL H.D., SAUER R.,
DEFTOS L.J., DAMSON B.F., HOGAN M.L., AUBACH G.D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
BONE AND PREVENTING THEIR RENAL EXCRETION.
CC EMBL: V00106; 683; -.
DR EMBL: J00023; G163641; -.
DR EMBL: J00024; G163643; -.
DR EMBL: J00024; E18249; ALR-SEQ.
DR EMBL: J00024; E18250; ALR-INIT.
DR EMBL: K01938; G163647; -.
DR EMBL: M25082; G163645; -.
DR PIR: A01334; PTBO.
DR PIR: A24949; A24949.
DR PROSITE: PS00335; PARATHYROID; 1.
RN HORMONE; SIGNAL.
CC SIGNAL 1 25
FT PROPEP 26 31 PARATHYROID HORMONE.
FT CHAIN 32 115 V -> G (IN REF. 4).
FT CONFLICT 106 106
SQ SEQUENCE 115 AA; 12980 MW; 673E85F2 CRC32;

Query Match 100.0%; Score 52; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 6.49e-01; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Db 55 LKRIOD 61
QY 1 LKRIOD 7

RESULT 2
ID PTH CANFA STANDARD; PRT; 115 AA.
AC P52212;
DC 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.
OS CANT'S FAMILIARIS (DOG).
OC EUKARYOTA; METAZOA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; CARNIVORA.
RN [1]
RN SEQUENCE FROM N.A.
RN TISSUE-PARATHYROID;
RA ROSOL T.J., STEINMEYER C.L., MCCADLEY L.K., GRONE A.,
DEWILLE J.W., CAPEN C.C.;
RL GENE 160-241-243(1995).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
BONE AND PREVENTING THEIR RENAL EXCRETION.
CC EMBL: U15662; G358916; -.
DR PROSITE: PS00335; PARATHYROID; 1.
KW HORMONE; SIGNAL.
FT SIGNAL 1 25 BY SIMILARITY.
FT PROPEP 26 31 BY SIMILARITY.
FT CHAIN 32 115 PARATHYROID HORMONE.
SQ SEQUENCE 115 AA; 12957 MW; 16D0EBC CRC32;

Query Match 100.0%; Score 52; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 6.49e-01; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Db 55 LKRIOD 61
QY 1 LKRIOD 7

MIRAGE
(TM)

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Msearch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:18:33 1998; Maspar time 3.62 Seconds
Tabular output not generated. 81.362 Million cell updates/sec

Title: >US-08-817-547A-34
Description: (1-7) from US08817547A.pep
Perfect Score: 52
Sequence: 1 LRRKLOD 7

Scoring table:
PAM 150
Gap 15

Searched: 140542 seqs 42109429 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 22.212; Variance 26.174; scale 0.849

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	52	100.0	105	10	063473	PARATHYROID HORMONE (F	8.70e-01
2	52	100.0	929	9	032491	PUTATIVE NG-ADRENINE S	1.46e+00
3	51	98.1	242	8	040970	PUTATIVE MADS-BOX FAMI	1.46e+00
4	51	98.1	242	8	P93468	MADS-BOX FAMILY TRANSC	1.46e+00
5	51	98.1	257	8	Q40700	BOX PROTEIN.	1.46e+00
6	48	92.3	398	8	004471	SIMILAR TO SACCCHAROMYC	6.55e+00
7	48	92.3	481	3	018255	COSMID C2709.	6.55e+00
8	47	90.4	133	9	P73817	HYPOHETICAL 15.4 KD P	1.07e+01
9	47	90.4	243	8	040969	PUTATIVE MADS-BOX FAMI	1.07e+01
10	47	90.4	360	9	029516	DNA PRIMASE, PUTATIVE.	1.07e+01
11	47	90.4	836	10	063618	ESPIN.	1.07e+01
12	46	88.5	122	9	P71288	HYPOHETICAL 18911 PRO	1.72e+01
13	46	88.5	122	9	032286	XYZC PROTEIN.	1.72e+01
14	46	88.5	134	9	P75679	FROM BASES 263572 TO 2	1.72e+01
15	46	88.5	231	1	005436	CAM KINASE II (FRAGMENT	1.72e+01
16	46	88.5	263	9	P96187	HRPG.	1.72e+01
17	46	88.5	316	9	056689	TRANSMEMBRANE TRANSCRI	1.72e+01
18	46	88.5	434	1	P78918	FISSION YEAST (FRAGMENT	1.72e+01
19	46	88.5	899	1	006132	CHROMOSOME XII COSMID	1.72e+01
20	46	88.5	1034	3	017117	M51.4 PROTEIN.	1.72e+01

RESULT	ID	SEQUENCE	ALIGNMENTS
1	063473	PRELIMINARY; PRT; 105 AA.	
2	063473	PRELIMINARY; PRT; 105 AA.	
3	063473	PRELIMINARY; PRT; 105 AA.	
4	063473	PRELIMINARY; PRT; 105 AA.	
5	063473	PRELIMINARY; PRT; 105 AA.	
6	063473	PRELIMINARY; PRT; 105 AA.	
7	063473	PRELIMINARY; PRT; 105 AA.	
8	063473	PRELIMINARY; PRT; 105 AA.	
9	063473	PRELIMINARY; PRT; 105 AA.	
10	063473	PRELIMINARY; PRT; 105 AA.	
11	063473	PRELIMINARY; PRT; 105 AA.	
12	063473	PRELIMINARY; PRT; 105 AA.	
13	063473	PRELIMINARY; PRT; 105 AA.	
14	063473	PRELIMINARY; PRT; 105 AA.	
15	063473	PRELIMINARY; PRT; 105 AA.	
16	063473	PRELIMINARY; PRT; 105 AA.	
17	063473	PRELIMINARY; PRT; 105 AA.	
18	063473	PRELIMINARY; PRT; 105 AA.	
19	063473	PRELIMINARY; PRT; 105 AA.	
20	063473	PRELIMINARY; PRT; 105 AA.	
21	063473	PRELIMINARY; PRT; 105 AA.	
22	063473	PRELIMINARY; PRT; 105 AA.	
23	063473	PRELIMINARY; PRT; 105 AA.	
24	063473	PRELIMINARY; PRT; 105 AA.	
25	063473	PRELIMINARY; PRT; 105 AA.	
26	063473	PRELIMINARY; PRT; 105 AA.	
27	063473	PRELIMINARY; PRT; 105 AA.	
28	063473	PRELIMINARY; PRT; 105 AA.	
29	063473	PRELIMINARY; PRT; 105 AA.	
30	063473	PRELIMINARY; PRT; 105 AA.	
31	063473	PRELIMINARY; PRT; 105 AA.	
32	063473	PRELIMINARY; PRT; 105 AA.	
33	063473	PRELIMINARY; PRT; 105 AA.	
34	063473	PRELIMINARY; PRT; 105 AA.	
35	063473	PRELIMINARY; PRT; 105 AA.	
36	063473	PRELIMINARY; PRT; 105 AA.	
37	063473	PRELIMINARY; PRT; 105 AA.	
38	063473	PRELIMINARY; PRT; 105 AA.	
39	063473	PRELIMINARY; PRT; 105 AA.	
40	063473	PRELIMINARY; PRT; 105 AA.	
41	063473	PRELIMINARY; PRT; 105 AA.	
42	063473	PRELIMINARY; PRT; 105 AA.	
43	063473	PRELIMINARY; PRT; 105 AA.	
44	063473	PRELIMINARY; PRT; 105 AA.	
45	063473	PRELIMINARY; PRT; 105 AA.	

RESULT	ID	SEQUENCE	ALIGNMENTS
1	063473	PRELIMINARY; PRT; 105 AA.	
2	063473	PRELIMINARY; PRT; 105 AA.	
3	063473	PRELIMINARY; PRT; 105 AA.	
4	063473	PRELIMINARY; PRT; 105 AA.	
5	063473	PRELIMINARY; PRT; 105 AA.	
6	063473	PRELIMINARY; PRT; 105 AA.	
7	063473	PRELIMINARY; PRT; 105 AA.	
8	063473	PRELIMINARY; PRT; 105 AA.	
9	063473	PRELIMINARY; PRT; 105 AA.	
10	063473	PRELIMINARY; PRT; 105 AA.	
11	063473	PRELIMINARY; PRT; 105 AA.	
12	063473	PRELIMINARY; PRT; 105 AA.	
13	063473	PRELIMINARY; PRT; 105 AA.	
14	063473	PRELIMINARY; PRT; 105 AA.	
15	063473	PRELIMINARY; PRT; 105 AA.	
16	063473	PRELIMINARY; PRT; 105 AA.	
17	063473	PRELIMINARY; PRT; 105 AA.	
18	063473	PRELIMINARY; PRT; 105 AA.	
19	063473	PRELIMINARY; PRT; 105 AA.	
20	063473	PRELIMINARY; PRT; 105 AA.	
21	063473	PRELIMINARY; PRT; 105 AA.	
22	063473	PRELIMINARY; PRT; 105 AA.	
23	063473	PRELIMINARY; PRT; 105 AA.	
24	063473	PRELIMINARY; PRT; 105 AA.	
25	063473	PRELIMINARY; PRT; 105 AA.	
26	063473	PRELIMINARY; PRT; 105 AA.	
27	063473	PRELIMINARY; PRT; 105 AA.	
28	063473	PRELIMINARY; PRT; 105 AA.	
29	063473	PRELIMINARY; PRT; 105 AA.	
30	063473	PRELIMINARY; PRT; 105 AA.	
31	063473	PRELIMINARY; PRT; 105 AA.	
32	063473	PRELIMINARY; PRT; 105 AA.	
33	063473	PRELIMINARY; PRT; 105 AA.	
34	063473	PRELIMINARY; PRT; 105 AA.	
35	063473	PRELIMINARY; PRT; 105 AA.	
36	063473	PRELIMINARY; PRT; 105 AA.	
37	063473	PRELIMINARY; PRT; 105 AA.	
38	063473	PRELIMINARY; PRT; 105 AA.	
39	063473	PRELIMINARY; PRT; 105 AA.	
40	063473	PRELIMINARY; PRT; 105 AA.	
41	063473	PRELIMINARY; PRT; 105 AA.	
42	063473	PRELIMINARY; PRT; 105 AA.	
43	063473	PRELIMINARY; PRT; 105 AA.	
44	063473	PRELIMINARY; PRT; 105 AA.	
45	063473	PRELIMINARY; PRT; 105 AA.	

Thu Jul 30 13:38:16 1998

US-08-817-547A-34.rsp

RA ROD J.I.
RL MICROBIOLOGY 141:0-0(0).
DR EMBL; U20247; G2317805; -
KW TRANSFERASE; METHYLTRANSFERASE.
SQ SEQUENCE 929 AA; 1064/4 MW; 4085E117 CRC32;

Query Match 100.0%; Score 52; DB 9; Length 929;
Best Local Similarity 100.0%; Pred. No. 8.70e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 42 LRRKLOD 48
Oy 1 LRRKLOD 7

Search completed: Thu Jul 30 11:19:10 1998
Job time : 37 secs.

WIDEORLH
(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:22:40 1998; MasPar time 2.49 Seconds
Tabular output not generated. 30.840 Million cell updates/sec

Title: >US-08-817-547A-36
Description: (1-5) from US08817547A.pep
Perfect Score: 39
Sequence: 1 LRKKL 5

Scoring table:
PAM 150
Gap 15

Searched: 124785 segs, 15338987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 14.364; Variance 43.704; scale 0.329

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	39	100.0	34	26	R62432 Accelerator peptide b	3.76e+02
2	39	100.0	34	9	R58040 [L8,Q18,A29,E30,I31]-	3.76e+02
3	39	100.0	34	8	R41551 [Thr16]hPTH (1-34).	3.76e+02
4	39	100.0	34	8	R41550 [D-Ala3]hPTH (1-34).	3.76e+02
5	39	100.0	34	9	R58034 Isopropyl-[L8,K]isopr	3.76e+02
6	39	100.0	34	9	R58228 [D-Asp3]-hPTH(1-34)-	3.76e+02
7	39	100.0	34	22	W20009 Cyclised [Nle 8,18, T	3.76e+02
8	39	100.0	34	22	W20003 Cyclised [Nle 8,18, T	3.76e+02
9	39	100.0	34	22	W17963 Human PTH analogue [C	3.76e+02
10	39	100.0	36	9	R58215 [D-Glu19]-hPTH(1-36)-	3.76e+02
11	39	100.0	36	9	R58057 [L8,D10,A16,Q18]-hPTH	3.76e+02
12	39	100.0	36	9	R58252 [Asn1]-hPTH(1-36)-NH2	3.76e+02
13	39	100.0	36	9	R58276 [Met(O2)18]-hPTH(1-36	3.76e+02
14	39	100.0	36	9	R58278 [D-Met18]-hPTH(1-36)-	3.76e+02
15	39	100.0	36	9	R58227 [D-Gln29]-hPTH(1-36)-	3.76e+02
16	39	100.0	36	9	R58298 [NMeVal15]-hPTH(1-36)	3.76e+02
17	39	100.0	36	9	R58297 [Pro35]-hPTH(1-36)-NH	3.76e+02
18	39	100.0	38	9	R58136 [Arg19]-hPTH(1-38)-OH	3.76e+02
19	39	100.0	38	9	R58108 [Arg14]-hPTH(1-38)-OH	3.76e+02

20	39	100.0	38	9	R58162 [Arg33]-hPTH(1-38)-OH	3.76e+02
21	39	100.0	38	9	R58101 [Gln13]-hPTH(1-38)-OH	3.76e+02
22	39	100.0	38	9	R58107 [Lys14]-hPTH(1-38)-OH	3.76e+02
23	39	100.0	38	9	R58029 [Leu1]-hPTH(1-38)-OH	3.76e+02
24	39	100.0	38	9	R58121 [Met17]-hPTH(1-38)-OH	3.76e+02
25	39	100.0	38	9	R58036 [Gln16]-hPTH(1-38)-OH	3.76e+02
26	39	100.0	44	26	P30015 Human parathyroid hor	3.76e+02
27	39	100.0	84	27	W25687 Human parathyroid hor	3.76e+02
28	39	100.0	84	4	R23397 Porcine parathyroid h	3.76e+02
29	39	100.0	84	4	R23472 Porcine parathyroid h	3.76e+02
30	39	100.0	84	4	R23472 Porcine parathyroid h	3.76e+02
31	39	100.0	84	4	R23379 Bovine parathyroid ho	3.76e+02
32	39	100.0	84	4	R23353 Bovine parathyroid ho	3.76e+02
33	39	100.0	84	5	R29567 Oxidation resistant l	3.76e+02
34	39	100.0	84	4	R21181 Human parathyroid hor	3.76e+02
35	39	100.0	84	4	R21180 Human parathyroid hor	3.76e+02
36	39	100.0	84	4	R21160 Human parathyroid hor	3.76e+02
37	39	100.0	84	4	R21161 Human parathyroid hor	3.76e+02
38	39	100.0	84	5	R28313 Human parathyroid hor	3.76e+02
39	39	100.0	84	4	R23356 Bovine parathyroid ho	3.76e+02
40	39	100.0	84	4	R23357 Bovine parathyroid ho	3.76e+02
41	39	100.0	84	4	R23466 Porcine parathyroid h	3.76e+02
42	39	100.0	84	4	R21191 Human parathyroid hor	3.76e+02
43	39	100.0	289	5	R28835 Vp1 Asp101Glu of HRV	3.76e+02
44	39	100.0	479	27	W27390 McH4 protein.	3.76e+02
45	39	100.0	496	27	W27391 McH5 protein.	3.76e+02

ALIGNMENTS

RESULT 1
ID R62432 standard; peptide; 34 AA.
AC R62432;
DT 31-JUL-1995 (first entry)
DE Accelerator peptide basic region peptide, P-8.
KW Accelerator; basic amino acid; cell growth factor; growth; gingiva;
KW periodontal tissue; regeneration; periodontitis; periodontal pocket;
KW down growth; epithelium; fibre adhesion; cement.
OS Synthetic.
PN J06234653.A.
PD 23-AUG-1994.
PR 10-FEB-1993; 04598.
PR 10-FEB-1993; JP-04598.
PA (SUNZ) SUNSTAR CHEM IND CO LTD.
DR WPI: 95-157631/21.
PT Accelerator for regenerating periodontal tissue - comprises
PT peptide having 3-34 aminoacid residues having connected basic
PT aminoacid residues
PS Disclosure: Page 3; 7pp; Japanese.
CC The sequences in R62425-36 are peptide fragments of an accelerator
CC protein which contain at least two basic amino acids. The accelerator
CC also comprises a cell growth factor. The accelerator may be used to
CC accelerate the growth of periodontal tissue regeneration. The
CC accelerator is applied by opening the gingiva, treating the tissue
CC destroyed by periodontitis and applying the accelerator in the
CC epithelium and pocket. The accelerator reduces the down growth of the
CC epithelium and accelerates fibre adhesion and regenerates cement.
SQ Sequence 34 AA;

Query Match 100.0%; Score 39; DB 26; Length 34;
Best Local Similarity 100.0%; Pred.No. 3.76e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 lrkkl 28
|||||
QY 1 LRKKL 5

RESULT 2
ID R58040 standard; peptide; 34 AA.
AC R58040;
DT 20-SEP-1994 (first entry)
DR [L8,Q18,A29,E30,I31]-hPTH(1-34)-OH.

KW Human parathyroid hormone; hPTH; variant; analogue;
 KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
 KW hypoparathyroidism.
 OS Synthetic.

PN GB2269176-A.
 PD 02-FEB-1994.
 PF 12-JUL-1993: 014384.
 PR 15-JUL-1992: GB-015009.
 PR 18-DEC-1992: GB-026415.
 PR 23-DEC-1992: GB-026859.
 PR 23-DEC-1992: GB-026861.
 PR 28-JAN-1993: GB-001691.
 PR 28-JAN-1993: GB-001692.
 PR 14-APR-1993: GB-007673.
 PR 19-APR-1993: GB-008033.
 PA (SANO) SANDOZ LTD.
 PA (BADE/) BAUER W.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 PA Albert R, Bauer W, Breckenridge R, Cardinaux F,
 Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
 Waelchli R, Rainer A;
 DR WPI: 94-018352/03.
 PT New active para-thyroid hormone variants - used for treating or
 preventing osteoporosis etc.
 PS Example 30; Page 36; 92pp; English.
 CC This peptide is an example of a highly generic formula covering
 parathyroid hormone variants useful for treating or preventing bone
 conditions associated with calcium depletion/resorption. In cases
 where calcium fixation is required (esp. osteoporosis) or to treat
 hypoparathyroidism.
 CC Sequence 34 AA;
 SQ

Query Match 100.0%; Score 39; DB 9; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.76e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 24 LrKkL 28
 11111
 QY 1 LrKkL 5

Search completed: Thu Jul 30 11:22:55 1998
 Job time : 15 secs.

W D S E I H
(TM)

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Search_pp protein - protein database search, using Smith-Waterman algorithm
in on: Thu Jul 30 11:22:05 1998; Maspar time 2.97 Seconds
Tabular output not generated. 61.502 Million cell updates/sec

Title: >US-08-817-547A-36
Description: (1-5) from US08817547A.pep
Perfect Score: 39
Sequence: 1 LRKKL 5

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

pl156
1:pl1 2:pl12 3:pl13 4:pl14 5:nr13d

Statistics: Mean 20.005; Variance 26.164; scale 0.765

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Suit No.	Score	Query Match	Length	ID	Description	Pred. No.
1	39	100.0	34	5 12WE	parathyroid hormone (1.53e+02
2	39	100.0	34	5 12WG	parathyroid hormone 4	1.53e+02
3	39	100.0	34	5 12WH	cyclic parathyroid ho	1.53e+02
4	39	100.0	34	5 12WA	parathyroid hormone (1.53e+02
5	39	100.0	34	5 12WF	parathyroid hormone 4	1.53e+02
6	39	100.0	35	5 12WD	parathyroid hormone (1.53e+02
7	39	100.0	36	5 12WB	parathyroid hormone (1.53e+02
8	39	100.0	37	5 12WP	parathyroid hormone f	1.53e+02
9	39	100.0	37	5 12WC	parathyroid hormone (1.53e+02
10	39	100.0	73	5 3FISA	Fis protein (factor f	1.53e+02
11	39	100.0	73	5 3FISB	DNA-binding protein f	1.53e+02
12	39	100.0	73	5 3FISC	DNA-binding protein f	1.53e+02
13	39	100.0	73	5 1FIPB	Fis protein (factor f	1.53e+02
14	39	100.0	74	5 1FICB2	Fis protein (factor f	1.53e+02
15	39	100.0	75	5 1FICB2	Fis protein (factor f	1.53e+02
16	39	100.0	89	5 1FICB2	Fis mutant K36E, cha	1.53e+02
17	39	100.0	271	5 1RUPA2	rhinovirus 14 mutant	1.53e+02
18	39	100.0	273	5 1RUCB	rhinovirus 14 mutant	1.53e+02
19	39	100.0	273	5 1RHVA	rhinovirus 14 (hrv14)	1.53e+02
20	39	100.0	273	5 1RHVA	rhinovirus 14 mutant	1.53e+02
21	39	100.0	273	5 1RHVA	rhinovirus 14 mutant	1.53e+02
22	39	100.0	273	5 1RHVA	rhinovirus 3 coat pro	1.53e+02
23	39	100.0	273	5 1VRHA	rhinovirus 14 mutant	1.53e+02

24	39	100.0	273	5 1RUEA	rhinovirus 14 mutant	1.53e+02
25	39	100.0	273	5 1RUDA	rhinovirus 14 mutant	1.53e+02
26	39	100.0	273	5 1RUDA	rhinovirus 14 mutant	1.53e+02
27	39	100.0	273	5 2R07A	coat protein VP1 (wit	1.53e+02
28	39	100.0	273	5 2R81A	coat protein VP1 (wit	1.53e+02
29	39	100.0	273	5 2R2A	coat protein VP1 (wit	1.53e+02
30	39	100.0	273	5 4R1VA	coat protein VP1, cna	1.53e+02
31	39	100.0	273	5 2R53A	coat protein VP1 (wit	1.53e+02
32	39	100.0	273	5 2R53A	coat protein VP1 (wit	1.53e+02
33	39	100.0	273	5 2R53A	coat protein VP1 (wit	1.53e+02
34	39	100.0	273	5 2R53A	coat protein VP1 (wit	1.53e+02
35	39	100.0	273	5 1R09A	coat protein VP1 (wit	1.53e+02
36	39	100.0	273	5 2R04A	coat protein VP1 (wit	1.53e+02
37	39	100.0	273	5 2R04A	coat protein VP1 (wit	1.53e+02
38	39	100.0	273	5 2R1A	coat protein VP1 (wit	1.53e+02
39	39	100.0	273	5 1R1A	rhinovirus 14 mutant	1.53e+02
40	39	100.0	273	5 1R1A	coat protein VP1 (wit	1.53e+02
41	39	100.0	273	5 1R1A	coat protein VP1 (wit	1.53e+02
42	39	100.0	492	5 1ECGA	glutamine phosphoribo	1.53e+02
43	39	100.0	492	5 1ECFA	glutamine phosphoribo	1.53e+02
44	39	100.0	500	5 1ECFB	glutamine phosphoribo	1.53e+02
45	39	100.0	500	5 1ECGB	glutamine phosphoribo	1.53e+02

ALIGNMENTS

RESULT	1	12WE	#type complete
ENTRY		parathyroid hormone (residues 4-37) - human	
TITLE		HPH(4-37)	
ALTERNATE_NAMES		structure of human parathyroid hormone fragment 4-37, NMR 10	
PDB_TITLE		structure of human parathyroid hormone fragment 4-37, NMR 10	
ORGANISM		#formal_name Homo sapiens #common_name man	
REFERENCE		A67860	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WE	
REFERENCE		TN001721	
#authors		Marx, U.C.	
#book		In Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996	
COMMENT		Resolution: not applicable	
KEYWORDS		Determination: NMR	
FEATURE		hormone	
15-25		#region helix (right hand alpha)	
SUMMARY		#length 34 #molecular-weight 4128 #checksum 5508	
Query Match		100.0%; Score 39; DB 5; Length 34;	
Best Local Similarity		100.0%; Pred. No. 1.53e+02;	
Matches		5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
DB	21	LRKKL 25	
Qy	1	LRKKL 5	
RESULT	2	12WG	#type complete
ENTRY		parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -	
TITLE		synthetic	
ALTERNATE_NAMES		n-succinyl-hp(4-37)	
PDB_TITLE		succinyl human parathyroid hormone 4-37, NMR, 10 structures	
ORGANISM		#formal_name synthetic	
REFERENCE		A67743	
#authors		Roesch, P.; Marx, U.C.	
#submission		submitted to the Brookhaven Protein Data Bank, June 1996	
#cross-references		PDB:12WG	
REFERENCE		TN003319	
#authors		Marx, U.C.	
#book		In Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996	
COMMENT		Resolution: not applicable	

COMMENT Determination: NMR
 KEYWORDS disease mutation; hormone; signal
 FEATURE 2-9
 15-25 #region helix (right hand alpha)\
 SUMMARY #region helix (right hand alpha)
 #length 34 #molecular weight 4128 #checksum 5508
 Query Match 100.0%; Score 39; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.53e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 21 LRKRL 25
 QY 1 LRKRL 5

Search completed: Thu Jul 30 11:22:22 1998
 Job time : 17 secs.

M I S E R I E (TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Jul 30 11:20:45 1998; Maspar time 2.01 Seconds
Tabular output not generated. 62.459 Million cell updates/sec

Title: >US-08-817-547A-36
Description: (1-5) from US08817547A.pep
Perfect Score: 39
Sequence: 1 LRKL 5

Scoring table: PAM 150
Gap 15

Searched: 69111 seqs, 25083644 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 21.052; Variance 21.024; scale 1.001

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Hit No.	Score	Query Match	Length	ID	Description	Pred. No.
1	39	100.0	98	1	FIS_ECOLI FACTOR-FOR-INVERSION S	4.38e+01
2	39	100.0	100	1	YI91_ECOLI INSERTION ELEMENT IS91	4.38e+01
3	39	100.0	112	1	YI91_SHIDY INSERTION ELEMENT IS91	4.38e+01
4	39	100.0	115	1	PTHY_CANPA PARATHYROID HORMONE PR	4.38e+01
5	39	100.0	115	1	PTHY_HUMAN PARATHYROID HORMONE PR	4.38e+01
6	39	100.0	115	1	PTHY_BOVIN PARATHYROID HORMONE PR	4.38e+01
7	39	100.0	209	1	VS10_ROTBS MINOR OUTER CAPSID PRO	4.38e+01
8	39	100.0	209	1	RR3_GRATE CHLOROPLAST 30S RIBOSO	4.38e+01
9	39	100.0	213	1	URK_MYCPN URIDINE KINASE (EC 2.7	4.38e+01
10	39	100.0	224	1	TCTD_SALTY TRANSCRIPTIONAL REGULA	4.38e+01
11	39	100.0	229	1	YXDU_BACSU HYPOHETICAL 26.6 KD S	4.38e+01
12	39	100.0	242	1	RSTA_ECOLI TRANSCRIPTIONAL REGULA	4.38e+01
13	39	100.0	310	1	SYNK_ARATH SYNTAXIN-RELATED PROTE	4.38e+01
14	39	100.0	330	1	YXAO_BACSU HYPOHETICAL 37.5 KD P	4.38e+01
15	39	100.0	334	1	VH05_YEAST HYPOHETICAL 37.9 KD P	4.38e+01
16	39	100.0	353	1	V613_MERJA PUTATIVE ENDONUCLEASE	4.38e+01
17	39	100.0	360	1	HIS8_LACIA HISTIDINOL-PHOSPHATE A	4.38e+01
18	39	100.0	366	1	STY_SULSO TYROSYL-TRNA SYNTHETAS	4.38e+01
19	39	100.0	435	1	MRP_MYCLE MRP PROTEIN HOMOLOG.	4.38e+01
20	39	100.0	437	1	SECY_STRGB PREPROTEIN TRANSLOCASE	4.38e+01
21	39	100.0	437	1	SECY_STRGB PREPROTEIN TRANSLOCASE	4.38e+01
22	39	100.0	437	1	SECY_STRSC PREPROTEIN TRANSLOCASE	4.38e+01
23	39	100.0	437	1	SECT_STRLI PREPROTEIN TRANSLOCASE	4.38e+01

RESULT	1	STANDARD;	PRT;	98 AA.
ID	FIS_ECOLI			
AC	P11028: P37404:			
DT	01-JUL-1989 (REL. 11, CREATED)			
DT	01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	FACTOR-FOR-INVERSION STIMULATION PROTEIN (HIN RECOMBINATIONAL ENHANCER			
DE	BINDING PROTEIN) (FIS PROTEIN).			
GN	FIS.			
OS	ESCHERICHIA COLI, AND SALMONELLA TYPHIMURUM.			
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;			
OC	ENTEROBACTERIACEAE.			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE.			
RC	SPECIES-E.COLI:			
RX	MEDLINE: 88217925.			
RA	JOHNSON R.C., BALB C.A., PEEFFER D., SIMON M.I.;			
RL	PROC. NATL. ACAD. SCI. U.S.A. 85:3484-3488(1988).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES-E.COLI:			
RX	MEDLINE: 88247997.			
RA	KOCH C., VANDERKERCKHOVE J., KAHMANN R.;			
RL	PROC. NATL. ACAD. SCI. U.S.A. 85:4237-4241(1988).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES-E.COLI:			
RX	MEDLINE: 93094136.			
RA	BALB C.A., OSUNA R., PERCUSON K.C., JOHNSON R.C.;			
RL	J. BACTERIOL. 174:8043-8056(1992).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES-E.COLI: STRAIN-K12 / MG1655:			
RA	BLATTNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;			
RL	SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES-S.TYPHIMURUM: STRAIN-LT2;			
RX	MEDLINE: 95238273.			
RA	OSUNA R., LIENAU D., HUGHES K.T., JOHNSON R.C.;			
RL	J. BACTERIOL. 177:2021-2032(1995).			
RN	[6]			
RP	FUNCTION.			
RC	SPECIES-E.COLI:			
RX	MEDLINE: 91006075.			
RA	ROSS W., THOMPSON J.F., NEWLANDS J.T., GOURSE R.L.;			
RL	EMBO J. 9:3733-3742(1990).			

24	39	100.0	444	1	PURA_STYV3	ADENYLOSUCINATE SYNTH	4.38e+01
25	39	100.0	451	1	TRPC_BUCAP	INOLE-3-GLYCEROL PHOS	4.38e+01
26	39	100.0	455	1	YVU6_YEAST	HYPOHETICAL 51.6 KD P	4.38e+01
27	39	100.0	459	1	NT4M_HYLLA	NADH-UBIQUINONE OXIDOR	4.38e+01
28	39	100.0	479	1	ICE8_HUMAN	CASPASE-8 PRECURSOR (E	4.38e+01
29	39	100.0	496	1	SRM_MOUSE	TYROSINE-PROTEIN KINAS	4.38e+01
30	39	100.0	496	1	RECO_BACSU	ATP-DEPENDENT DNA HELI	4.38e+01
31	39	100.0	501	1	UVS2_NEUCR	UVS-2 PROTEIN.	4.38e+01
32	39	100.0	504	1	PUR1_ECOLI	AMIDOPHOSPHORIBOSYLTRA	4.38e+01
33	39	100.0	517	1	PUR1_HUMAN	AMIDOPHOSPHORIBOSYLTRA	4.38e+01
34	39	100.0	517	1	PUR1_RAT	NUCLEOPORIN NUP85 (NDC	4.38e+01
35	39	100.0	744	1	N083_YEAST	KINESIN-LIKE PROTEIN B	4.38e+01
36	39	100.0	745	1	KATC_ARATH	KINESIN-LIKE PROTEIN C	4.38e+01
37	39	100.0	754	1	RR3_CHLEU	CHLOROPLAST PUTATIVE 3	4.38e+01
38	39	100.0	800	1	SYEB_MYCGE	PHENYLALANYL-TRNA SYN	4.38e+01
39	39	100.0	806	1	POOL_HATIN	PROBABLE ZINC PROTEASE	4.38e+01
40	39	100.0	926	1	RAD2_YEAST	DNA REPAIR PROTEIN RAD	4.38e+01
41	39	100.0	1031	1	Y053_CABEL	HYPOHETICAL 117.1 KD	4.38e+01
42	39	100.0	1032	1	POLN_EEYVP	NONSTRUCTURAL POLYPROT	4.38e+01
43	39	100.0	2492	1	POLN_EEYV3	NONSTRUCTURAL POLYPROT	4.38e+01
44	39	100.0	2492	1	POLN_EEYVT	NONSTRUCTURAL POLYPROT	4.38e+01
45	39	100.0	2492	1	POLN_EEYVT	NONSTRUCTURAL POLYPROT	4.38e+01

RN [7]
RP FUNCTION.
RX MEDLINE; 96433150.
RA WOLD S., CROOKE E., SKARSTAD K.;
RL NUCLEIC ACIDS RES. 24:3527-3532(1996).
RN [8]
RP MUTAGENESIS, AND DOMAINS.
RC SPECIES-E.COLI;
RX MEDLINE; 9122411.
RA OSUNA R., FINKEL S.E., JOHNSON R.C.;
RL EMOA J. 10:1593-1603(1991).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC SPECIES-E.COLI;
RX MEDLINE; 91095026.
RA KOSTREVA D., GRANZIN J., KOCH C., CHOE H.-W., RAGHUNATHAN S., WOLF W.,
RA LABAHN J., KAHNANN R., SAENGER W.;
RL NATURE 349:178-180(1991).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC SPECIES-E.COLI;
RX MEDLINE; 92318262.
RA KOSTREVA D., GRANZIN J., STOCK D., CHOE H.-W., LABAHN J., SAENGER W.;
RL J. MOL. BIOL. 226:209-226(1992).
CC -1- FUNCTION: ACTIVATES RIBOSOMAL RNA TRANSCRIPTION. PLAYS A DIRECT
CC ROLE IN UPSTREAM ACTIVATION OF RNA PROMOTERS. BINDS TO A
CC RECOMBINATIONL ENHANCER SEQUENCE THAT IS REQUIRED TO STIMULATE
CC HIN-MEDIATED DNA INVERSION. PREVENTS INITIATION OF DNA REPLICATION
CC FROM ORIC.
CC -1- SUBUNIT: HOMODIMER.
DR EMBL; J03245; G145971; -;
DR EMBL; J03816; G145973; -;
DR EMBL; M95784; G145977; -;
DR EMBL; U18987; G606202; -;
DR EMBL; AE000405; G1789661; -;
DR PIR; U03101; G424092; -;
DR PIR; A32142; DNECRS.
DR PIR; A28207; A28207.
DR PIR; S15344; S15344.
DR PIR; C47043; C47043.
DR PDB; 1F1A; 31-OCT-93.
DR PDB; 1F1P; 14-FEB-95.
DR PDB; 3FIS; 31-OCT-93.
DR PDB; 4FIS; 31-OCT-93.
DR ECGENE; EG10317; FIS.
DR STYGENE; SG10100; FIS.
KW DNA-BINDING; 3D-STRUCTURE.
FT DOMAIN 17 44
FT DNA_BIND 74 93
FT HELIX 27 40
FT TURN 41 41
FT TURN 43 44
FT HELIX 50 70
FT TURN 71 72
FT HELIX 74 81
FT TURN 82 82
FT HELIX 85 94
FT TURN 95 96
SQ SEQUENCE 98 AA; 11240 MW; 6AE88082 CRC32;
REQUIRED FOR THE STIMULATION OF HIN-MEDIATED RECOMBINATION.
H-T-H MOTIF.
Query Match 100.0%; Score 39; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.38e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 88 LRKRL 92
QY 1 LRKRL 5
RESULT 2
ID Y191_ECOLI STANDARD; PRT; 100 AA.
AC P39212;

DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE INSERTION ELEMENT IS911 HYPOTHETICAL 11.6 KD PROTEIN (O100).
OS ESCHERICHIA COLI.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC ENTEROBACTERIACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE; 95334362.
RA BURLAND V.D., PLUNKETT G. III, SOFIA H.J., DANIELS D.L.,
RA BLATTNER F.R.;
RL NUCLEIC ACIDS RES. 23:2105-2119(1995).
DR EMBL; U14003; G537124; -;
DR EMBL; AE000499; G1790735; -;
KW HYPOTHETICAL PROTEIN; TRANSDUCIBLE ELEMENT.
SQ SEQUENCE 100 AA; 11558 MW; 3827E6B9 CRC32;
Query Match 100.0%; Score 39; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 4.38e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 82 LRKRL 86
QY 1 LRKRL 5
Search completed: Thu Jul 30 11:20:51 1998
Job time : 6 secs.

Thu Jul 30 13:38:17 1998

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DR EMBL: M54875; G601933; -
FT NON_TER 1
SQ SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;

Query Match 100.0%; Score 39; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.95e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 45 LKKL 49
1 LKKL 5
Qy 1 LKKL 5

Search completed: Thu Jul 30 11:21:47 1998
Job time : 37 secs.